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RESULT 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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GO; GO:000588; F:transmembrane receptor activity; TAS.
GO; GO:000488; F:transmembrane receptor activity; TAS.
GO; GO:0007155; P:cell adhesion; TAS.
GO; GO:0007165; P:signal transduction; TAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR007598; Ig_C2.
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CARBOHYD
CONFLICT
                             VGR3 MOUSE STANDARD; PRT; 1363 AA.
P35917;
01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Vascular endothalial growth factor receptor 3 precursor
(VEGFR-3) (Tyrosine-protein kinase receptor FLT4).
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DOMAIN
                FLT4
                                                                                                                                             MOUSE
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SMART; SM00408; IGC2; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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   musculus
                   OR FLT-4
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                                                                                                                                                                                                        GSP-AEPIPGRQGWVSSSLTLKVTSALSRDGISC
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                                                                                                                                                                                                                                                                                                                                                                   PGSSPSVQC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGDTVQLLCRGDGSPSPEYTL------FRLQDEQEEVLNVNLEGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGN
                                                                                                                                                                                                                                                                     PVLSRTONFTLLVQGSPELKTAEIEPKADGSWREGDEVTLICSARGH--
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67374 MW;
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   (Mouse)
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IG-LIKE V-TYPE 2.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
IG-LIKE C2-TYPE 3.
PROBABLE.
OF CICNAC.
N-LINKED (GLCNAC.
N-LINKED (GLCN
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3; Mismatches
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EXTRACELLULAR (POTENTIAL)
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
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MOIECLIAR, MORRIS J.C., Sookdeo H., Turner K.J., Molecular cloning of murine FLT and FLT4;"; Oncogene 8: 2293-2298(1993).
entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=C57BL/6J;
MEDLINE=93330572;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                                               tyrosine phosphate.
SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: EXPRESSED IN ADULT LUNG AN
FETAL LIVER, BRAIN, INTESTINE AND PLACENTA.
SIMILARITY: Belongs to the Tyr family of prote
CSF-1/PDGF receptor subtamily.
                 s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - Buropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way ified and this statement is not removed. Usage by and for commercial ities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                SIMILARITY: Contains 7 immunoglobulin-like C2-type domains
                                                                                                                                                                                                                                                                                                                                                                         CATALYTIC ACTIVITY: ATP + a
                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: RECEPTOR
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eher K., Morris G.
.C., Sookdeo_H., 1
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DR GG) GO:005515; Figt.

BR GG) GO:005515; Figrotein binding; IPI.

BR InterPro; IPR007110; Ig-like.

BR InterPro; IPR003598; Ig\_c2.

BR InterPro; IPR001214; RecepttyrkinsIII.

BR InterPro; IPR001245; Tyr\_pkinase.

BR InterPro; IPR001245; Tyr\_pkinase.

BR InterPro; IPR001266; Tyr\_pkinase\_AS.

BR InterPro; IPR001266; Tyr\_pkinase\_AS.

BR InterPro; IPR001266; Tyr\_pkinase\_AS.

BR Ffam; PP00047; ig; 5.

BR Ffam; PP00069; pkinase; 1.

BR PF0Dom; PD000001; Prot kinase; 2.

BR Ffam; PP00069; pkinase; 1.

BR PRODOM; PD000001; PROTEIN\_KINASE\_ATP; 1.

BR PROSITE; PS00107; PROTEIN\_KINASE\_DOM; 1.

BR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.

BR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.

BR PROSITE; PS00109; RRCEPTOR TYR KIN III; 1.

BR PROSITE; PS00240; RECEPTOR TYR KIN III; 1.

BR PROSITE; PS00240; RECEPTOR TYR KIN III; 1.

BR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.

BR PROSITE; PS00109; RRCEPTOR TYR KIN III; 1.

BR PROSITE; PS00109; RRCEPTOR TYR KIN III; 1.

BR PROSITE; PS00109; RRCEPTOR TYR KIN III; 1.

BR PROSITE; PS00109; PROTEIN\_KINASE; Phosphorylation; ATP-binding; KW Receptor; Transmembrane; Signal; Immunoglobulin domain; Repeat; KW Receptor; Transmembrane; Signal; Immunoglobulin domain; Repeat; Receptor; Tran Glycoprotein. SIGNAL CHAIN 2 EMBL; L07296; AAA40077.1; PIR; I58375; I58375. HSSP; P11362; 1FGK. 24 1363 775 1363 118 213 326 415 552 671 764 1173 859 879 1037 POTENTIAL.

VASCULAR ENDOTHELIAL GROWTH
RECEPTOR 3.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 4.
IG-LIKE C2-TYPE 5.
IG-LIKE C2-TYPE 5.
IG-LIKE C2-TYPE 7.
PROTEIN KINASE.
ATP (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY. ENDOTHELIAL GROWTH

VGR3

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MOD RES CARBOHYD

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Oncogene 15:691-700(1997).

-I-FUNCTION: May be involved as a regulatory protein in the transition of undifferentiated proliferating cells to the differentiated state. May also function as a cell adhesic molecule in a broad spectrum of embryonic and adult tissu-I-SUBCELLULAR LOCATION: Type I membrane protein.
-I-ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=5; Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NEO1 MOUSE
P97798;
16-OCT-2001
                                                                                                                                                                                        MEDLINE=97407661; PubMed=9264410; Keeling S.L., Gad J.M., Cooper H.M.; "Mouse neogenin, a DCC-like molecule, expressed widely in the adult mouse aroncogene 15:691-700(1997).
                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                       TISSUE=Brain;
                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
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16-OCT-2001 (Rel. 40, Last seq
10-OCT-2003 (Rel. 42, Last ann
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                                                                                                                                                                                                                                                                                                                                                                                                                            Neogenin
                                    Name=1;
                     IsoId=P97798-1;
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                                                                                                                                                                                                                                                                                                                                                                                                                            precursor.
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Last annotation updat
                     Sequence=Displayed
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Pred. No. 1
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     HSSP; P02751; ITTE.
HSSP; P02751; ITTE.
MGD; MGI:1097159; Neol.
InterPro; IPR008957; FN_III-like.
InterPro; IPR003961; FN_III
InterPro; IPR003962; FnIII subd.
InterPro; IPR003598; Ig_c2.
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PFANTS; PR00014; FNTYPEIII.

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Note=Expression developmentally regulated;
TISSUE SPECIFICITY: Widely expressed.
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SIMILARITY: Belongs to the immunoglobulin superfamily.
SIMILARITY: Contains 4 immunoglobulin-like C2-type dom
SIMILARITY: Contains 6 fibronectin type III domains.
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IsoId=P97798-3;
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01-OCT-1989 (Rel. 12, Created)
O1-OCT-1989 (Rel. 12, Last sequence update)
O1-OCT-2003 (Rel. 42, Last annotation update)
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VARSPLIC
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MEDLINE-88024987; PubMed=2959318;

Kinet J.-P., Metzger H., Hakimi J., Kochan

Kinet J.-P., Metzger H., Hakimi J., Kochan

"A cDNA presumptively coding for the alpha

with high affinity for immunoglobulin E.";

Biochemistry 26:4605-4610(1987).
SEQUENCE OF 21-245
MEDLINE=88289772; E
                                                                                                                                    MEDLINE-88158102; PubMed=2964640;
Shimizu A., Tepler I., Benfey P.N.,
                                                                                                                                                                                SEQUENCE FROM N.A. TISSUE=Mast cells;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus
                                                        "Human and rat mast cell high-affinity immunoglobulin characterization of putative alpha-chain gene products Proc. Natl. Acad. Sci. U.S.A. 85:1907-1911(1988).
                                                                                                                                                                                                                                             Submitted (MAR-1988)
                                                                                                                                                                                                                                                                Kochan J
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Sciurognathi; Muridae;
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DOMAIN
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EMBL; J03606; AAA41582.1; --
EMBL; M21622; AAA41146.1; --
PIR; C31327; A30154.
HSSP; P12319; 1ALS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Proc. Natl. Acad. Sci. U.S.A. 85:5639-5643 (1988).

-I-FUNCTION: BINDS TO THE FC REGION OF IMMUNOGLOBULINE EPSILO.

AFFINITY RECEPTOR. RESPONSIBLE FOR INITIATING THE ALLERGIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Liu
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IgE-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00047; ig; 2.
SMART; SM00409; IG; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR007110; Ig-like InterPro; IPR003599; Ig.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "cDNA heterogeneity suggests structural variants related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mmunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESPONSE. BINDING OF ALLERGEN TO RECEPTOR-BOUND IGE LEADS ACTIVATION AND THE RELEASE OF MEDIATORS (SUCH AS HISTAMINE RESPONSIBLE FOR THE MANIFESTATIONS OF ALLERGY THE SAME REASO INDUCES THE SECRETION OF IMPORTANT LYMPHOKINES. SUBGUNIT: TETRAMER OF AN ALPHA CHAIN, A BETA CHAIN, AND TWO DISULFIDE LINKED GAMMA CHAINS.

SUBCELLULAR LOCATION: Type I membrane protein.

SIMILARITY: Contains 2 immunoglobulin-like domains.
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                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PS50835; IG_LIKE; 1.
ling protein; Receptor;
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                                   GGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKID
                                                                                                                                                                                                                                                                           LLVLQLALLPAATQGNKVVLGK-----KGDTVELTC---TASQKKSIQFHWKNSNQIKI
DSNNISIRKATFNDSGSYHCTGYLN--KVECKSD
                                                                                                               LLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRG---
                                                                                                                                                                                              LGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVED--QKEEVQ
                                                                                                                                                                                                                                        LVLISLGVMLTATQKSVVSLDPPWIRILTGDKVTLICNGNNSSQMNSTK--WIHNDSI--
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23.4%;
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                                                                                                                                                         -SNVKSSHW-----VIVSATIQDSGKYICQKQGFYKSKPVY
                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNA
                                                                                                                                                                                                                                                                                                                                   Score 95;
Pred. No.
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CYTOPLASMIC (POTENTIAL)
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N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
A0E67DD363B72197 CF
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Mismatches
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(GLCNAC.
                                                                            -GSFDIRCRSWKKWKVHKVIYYKDDIAFKYSY
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                                                                                                                                                                                                                                                                                                                                                     Length
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RESULT 97
VGR2_HUMAN
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P33968; O60723; Q14178;
01-JUN-1994 (Rel. 29, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Vascular endothelial growth factor receptor 2 precursor (EC 2.7.1.112)
(VEGFR-2) (Kinase insert domain receptor) (Protein-tyrosine kinase receptor F1k1).
KDR OR FLK1. ''........
                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                            Terman B.I., Dougher-Vermazen M., Carrion M.E., Dimitrov D.,
Armellino D.C., Gospodarowicz D., Boehlen P.;
"Identification of the KDR tyrosine kinase as a receptor for vascuendothelial cell growth factor.";
Biochem. Biophys. Res. Commun. 187:1579-1586 (1992).
Biochem. Biophys. Res. Commun. 187:1579-1586 (1992).
-I- FUNCTION: RECEPTOR FOR VEGF- OR VEGF-C. HAS A TYROSINE-PROTEIN KINASE ACTIVITY. THE VEGF-KINASE LIGAND/RECEPTOR SIGNALING SYSTANCHING BEGULATION OF PLAYS A KEY ROLE IN VASCULAR DEVELOPMENT AND REGULATION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-22 FROM N.A. MEDLINE=96032749; PubMed=7559454; Parterson C., Perrella M.A., Hsie
                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION.
MEDLINE=93038639; PubMed=1417831;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tyrosine kinase.";
Oncogene 6:1677-1683(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Umbilical vein;
MEDLINE=92019839; PubMed=1656371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Umbilical vein;
Yu Y., Whitney R.G., Sato J.D.;
"Coding region for human VEGF receptor KDR (VEGFR-2).";
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yin L.Y., Wu Y., Patt
"Full length human KI
Submitted (DEC-1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
EMBL; AF035121; AAB88005.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Identification of a new endothelial cell growth tyrosine kinase.";
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                                                                                                                                                                     tyrosine phosphate.
SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: Belongs to the Tyr family of protein kinases.
CSF-1/PDGF receptor subfamily.
SIMILARITY: Contains 7 immunoglobulin-like C2-type domains.
                                                                                                                                                                                                                                                             VASCULAR PERMEABILITY.
CATALYTIC ACTIVITY: ATP + a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and functional analysis of the promoter for KDR/flk-1,
for vascular endothelial growth factor.";
Chem. 270:23111-23118(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .I., Carrion M.E.,
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an KDR/flk-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         terson C.;
DR/flk-1 sequence.";
to the EMBL/GenBank/DDBJ databases.
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EMBL; AF063658; AAC16450.1; -
EMBL; X61656; CAA43837.1; -
EMBL; L04947; AAA59459.1; -
EMBL; X99776; CAA61916.1; -
PIR; JC1402; JC1402.
HSSP; P11362; 1FGK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MIM; 191306; -.

GO; GO:0005887; C:integral to plasma membrane; TAS.

GO; GO:0005021; F:vascular endothelial growth factor receptor.

GO; GO:0007169; P:transmembrane receptor protein tyrosine kin.

InterPro; IPR007110; Ig-1ike.

InterPro; IPR007110; Ig-1ike.

InterPro; IPR00719; Prot kinase.

InterPro; IPR001824; RecepttyrkinsIII.

InterPro; IPR001824; Tyr_pkinase.

InterPro; IPR001245; Tyr_pkinase_AS.
                CARBOHYD
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MOD_RES
CONFLICT
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SMART; SM00408; IGC2; 2.

SMART; SM00219; TyrKc; 1.

PROSITE; PS50835; IG LIKE; 5.

PROSITE; PS00107; PROTEIN KINASE ATP; 1.

PROSITE; PS00101; PROTEIN KINASE DOM; 1.

PROSITE; PS00101; PROTEIN KINASE TYR; 1.

PROSITE; PS00104; PROTEIN KINASE TYR; 1.

PROSITE; PS00105; PROTEIN KINASE TYR; 1.

PROSITE; PS00104; RECEPTOR TYR KIN III; 1.

PROSITE; PS00240; RECEPTOR TYR KIN III; 1.

PROSITE; PS00240; RECEPTOR TYR KIN III; 1.
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CARBOHYD
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Pfam; PF00069; pkinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genew;
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                  $
AMED (GLCNAL

AMED (GLCNAC...)

ALINKED (GLCNAC...)

ALINKED (GLCNAC...)

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score 95; DB 1; pred. No. 20;

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nss; rouse; in extracellular; NAS.
GO; GO:0005576; C:entrigen binding; NAS.
GO; GO:0003823; F:antrigen response; NAS.
GO; GO:0006855; p:immune response; NAS.
GO; GO:0006855; p:immune response; NAS.
GO; GO:0006855; p:immune
GO; reponses; ig\_v.
InterPro; IPRO03596; Ig\_v.
InterPro; NAO(4067; IG; I.XE; I.
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PROSITE; PS50835; ITME; I.
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"Chemical structure of 2 kappa-type Bence Jones proteins (Cum.).";

Hoppe-Seyler's Z. physiol. Chem. 348:1077-1080(1967)

REVISIONS TO 39 AND 41. H.U., Hess M., Le REVISIONS TO 39 AND 41. H.U., Watanabe S. Hilschmann N., Barnikol H.U., Watanabe S. Steinmer. Kayne M., Suter L., Watanabe S. Steinmer. Kayne M., Shugar D. (eds.);
Steinmer. Kayne M., Shugar D. (eds.);
Gamma globulins: structure and function,
Gamma globulins: structure and function.

NCBI\_TaxID=9606;

page

Length 108,

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28

its content Usage by a

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Q62556; P97392;
01-NOV-1997 (Re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
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SEQUENCE
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TRANSMEM
                                                                                                                                                                                                                                                           Ishii T., Aoki N., Noda A., Adachi T., Nakamura R., Matsuda T., "Carboxy-terminal cytoplasmic domain of mouse butyrophilin specifically associates with a 150-kDa protein of mammary epithecells and milk fat globule membrane.";
                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=129; TISSUE=Mammary gland;
MEDLINE=97148936; PubMed=8995761;
Ogg S.L., Komaragiri M.V.S., Mather I.H.;
"Structural organization and mammary-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUL-1998 (Rel. 36, Last
15-MAR-2004 (Rel. 43, Last
Butyrophilin precursor (BT)
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                      TISSUE=Mammary gland;
MEDLINE=96125722; PubMed=8541302;
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 39-487 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                               butyrophilin gene.";
Mamm. Genome 7:900-905(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BTN1A1 OR BTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHAIN
                                                                                                                                                                                                                                                  Biochim.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                              association of cytoplasmic droplets with the apical plasma membrane (By similarity).

SUBUNIT: Seems to associate with xanthine dehydrogenase/oxidase.

SUBCELLULAR LOCATION: Type I membrane protein.

TISSUE SPECIFICITY: Expressed in mammary tissue and secreted in association with the milk fat-globule membrane during lactation.

DEVELOPMENTAL STAGE: Expression increases during the last half of pregnancy and is maximal during lactation.

SIMILARITY: Belongs to the immunociation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                          SIMILARITY: Contains 2 immunoglobulin-like
                                                                                                                                                                                                     chim. Biophys. Acta 1245:285-292 (1995).

FUNCTION: May function in the secretion of milk-fat may act as a specific membrane-associated receptor f association of cytoplasmic droplets with the animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQ-CRSPRGKNIQG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QAPSSDSHHEFLALWDSAKGTIHSEEVEQEKVAVFRDASRFILNLTSVKPEDSGIYFCMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QIKILGNQGSFL----TKGPSKLNDRADSRRSLW-DQGNFPLIIKNLKIEDSDTYICEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LLLAAQLAVLHGSSVLQQTPAYIKVQTNKMVM-----LSCEAKISLSNMRIYWLRQR
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171
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210 AA;
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annotation update)
(Butyrophilin subfamily 1 member A1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T-CELL SURFACE GLYCOPROTEIN CD8 BETA CATRACELLULAR (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; I
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                            expression of
                                                          V-type
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Murinae; Mus
                                                            domains
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Pfam; PF00622; SPRY; 1.
SMART; SM00406; IGv; 1.
SMART; SM00589; PRY; 1.
SMART; SM00449; SPRY; 1.
PROSITE; PS50835; IG_LIKE; 2
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CONFLICT
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SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                               130 NDDFEEAAVYLKVAAVGSDPQISMTVQENGEMELECTSSGWYPEPQVQWRTGNREMLPST
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                                                                                                                                                                                                                                                                                                                                                                    11 LLVLQLALLPAA-----TQGNKVVLGKKGDTVELTCTASQKKSIQF----HWKNSNQIKI
                                                                                                                                                                                                                                                                                                                                                                                                            62;
                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 22.:
62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              p; IPR001870; B302.
p; IPR007110; Ig-like.
p; IPR003596; Ig-v.
p; IPR006574; PRV.
p; IPR003877; SPRY_receptor.
                                    PTGSALPDPQTASALPDPPAASALPAALAVISFLLGLG
                                                                            SESKKHNEEGLFTVAVSMM-IRDSSIKNMSCCIQNILLGQGKEVEI-
                                                                                                                     --PRGKNIQGGKTLSVSQLELQDSG--TWTCTV----LQNQKKVEFKIDIVPRASALPAP
                                                                                                                                                                                                    ----QKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGS----SPSVQCRS---
                                                                                                                                                                                                                                              LLYRDGQEQEGQQMTEYRGRATL ---- ATAGLLD-
                                                                                                                                                                                                                                                                      L-----GNQGSFLT--KGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVED
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SLPAPFVPRLTPWIVAVAIILLALG
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                                                                                                                                                                                                                                                                                                                                                                                                            42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL).

IG-LIKE V-TYPE 1.

IG-LIKE V-TYPE 1.

IG-LIKE V-TYPE 2.

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

V -> FOR (IN REF. 2).

E -> D (IN REF. 2).

E -> S (IN REF. 2).

V -> FF (IN REF. 2).

SL -> FF (IN REF. 2).

PRRV -> LAFY (IN REF. 2).

CHOLONGE CONTOUR COLUMN COLUMN
                                                                                                                                                                                                                                                                                                                                                                                                                               Score 94.5;
Pred. No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Immunoglobulin domain; Signal; Repeat.
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EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NI)
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333F4DE2C7704480 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB
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Oshyv2 sus scrofa
P79921 xenopus lae
P70193 mus musculu
O97394 drosophila
O9jlm2 rattus morv
O9w6v2 gallus gall
O44924 drosophila
O8aw/9 brachydanio
O8aw80 brachydanio
O93y8 homo sapien
O80224 mus musculu
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Q92626 homo sapien
Q8nfp4 homo sapien
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Q8iv49 homo sapien
Q8iv29 homo sapien
Q8blk3 mus musculu
Q8ta95 homo sapien
Q8uv81 brachydanio
Q9h1x9 homo sapien
Q9uv64 drosophila
Q9cr4 drosophila
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GO; GO:0016020; C:membrane; IEA.
GO; GO:0006955; P:immune response; II
InterPro; IPR000973; CD4 TCA9.
InterPro; IPR007110; Ig-Tike.
InterPro; IPR007110; Ig-V.
Pfam; PF00047; ig: 2.
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                                                                                                                                                                                                      Corbet S., Barre-Sinoussi F., Allan J.S.;
"Relation between phylogeny of African green monkey CD4
their respective simian immunodeficiency virus genes.";
J. Med. Primatol. 26:120(1997).
                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Cercopithecus.
                                                                                                                                                                                                EMBL; AF001225; AAB60872.1;
                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=98017879; PubMed=9379478;
                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=60711;
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            PRINTS; PR00692
SMART; SM00406;
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Matches 148
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009262;
01-JUL-1997
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GO; GO:0006955; P:immune response;
InterPro; IPR000973; CD4 TCAg.
InterPro; IPR007110; Ig-Tike.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIINE=98017879; PubMed=9379478; Fomsgaard A., Muller-Trutwin M.C., Diop O., Hansen J., Ne Corbet S., Barre-Sinoussi F., Allan J.S.; Corbet S., Berre-Sinoussi F., Allan J.S.; "Relation between phylogeny of African green monkey CD4 their respective simian immunodeficiency virus genes."; J. Med. Primatol. 26:120-128(1997).

EMBL; AF001221; AAB60868.1; -.
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Mammalia; Eutheria; Primates; (
Cercopithecinae; Cercopithecus.
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01-JUL-1997 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                            SMART;
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                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50835;
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; PR00692; CD-1
; PR006; IGV; 1
                                                                                                                                                                                                                                                                                                                                                                                                                              SM00406;
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GSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIV
                                                                  VVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLW
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397 AA;
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                                                                                                                                                                                                                                         58.2%; Score 767; DB 6; ilarity 85.5%; Pred. No. 1.2e-58; Conservative 10; Mismatches 15
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GO; GO:0006955; P:immune response;
InterPro; IPR000973; CD4 TCA9.
InterPro; IPR007110; Ig-Tike.
InterPro; IPR003596; Ig_v.
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Cercopithecinae; Cercopithecus.
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397 AA;
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Pfam; PF00047; 19; 2.
PRINTS; PR00692; CD4TCANTIGEN.
SMART; SM00406; IGv; 1.
SMART; SM00406; IGV; 1.
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GO; GO:0016020; C:membrane; IEA.
GO; GO:0006955; P:immune response; I:
GO; GO:0006955; P:immune response; I:
InterPro; IPR0007110; Ig-Tike.
InterPro; IPR001596; Ig_v.
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GO; GO:0016020; C:membrane; IEA.
GO; GO:0006955; P:immune response;
InterPro; IPR000973; CD4 TCAg.
InterPro; IPR007110; Ig-Tike.
InterPro; IPR003596; Ig_v.
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Corbet S., Barre-Sinoussi F., Allan J.S.;
"Relation between phylogeny of African green monkey
their respective simian immunodeficiency virus genes
J. Med. Primatol. 26:120-128(1997).
                                                                                                                                                                                                                                                                        EMBL; AF001223; AAB60870.1;
                                                                                                                                                                                                                                                                                            Corbet S., Barre-Sinoussi F., Allan J.S.; "Relation between phylogeny of African green monkey their respective simian immunodeficiency virus genes J. Med. Primatol. 26:120-128(1997).
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MEDLINE=98017879; PubMed=9379478;
Fomsgaard A., Muller-Trutwin M.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=60711;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cercopithecinae; Cercopithecus.
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Mammalia; Eutheria; Primates;
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Pred. No. 1.2e-58;
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Allan J.S.;
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Catarrhini; Cercopithecidae;
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MEDLINE=980.17879; PubMed=9379478;

FOMSGBARD A. Muller-Trutwin M.C., Diop O., Hansen J., M.

Corbet S., Barre-Sinoussi F., Allan J.S.;

"Relation between phylogeny of African green monkey CD4

their respective simian immunodeficiency virus genes.";

J. Med. Primatol. 26:120-128(1997).
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GO; GO:0006955; P:immune response;
InterPro; IPR000973; CD4 TCA9.
InterPro; IPR007110; Ig-Tike.
InterPro; IPR003596; Ig_v.
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GSSPSVKCRSPRGKNIQGGRTLSVPQLERQDSGTWTCNVSQDQNTVEFKIDIV
                                 GSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIV 200
                                                                                       DQGCFSMIIKNLKIEDSETYICEVENKEEEVELLVFGLTANSDTHLLQGQSLTLTLESPP
                                                                                                                                     DQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPP 147
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Pred. No. 2.6e-58;
                                                                                                                                                                                                                                                                                                     Score 763;
Pred. No. 2.
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C: SUBGUNIT: ASSOCIATES WITH P56-LCK (BY SIMILARITY).

C: SUBGULLLAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).

C: SUBGULLAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).

C: SUBGULLARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERPAMILY. CONTAINS.

C: ONE V-LIKE AND 3 C2-LIKE DOMAINS.

EMBL; AF00122; AAB60873.1; -.

SR EMBL; AF00122; AAB60873.1; -.

SR EMBL; AF00130; AAC25124.1; -.

DR HSSP; P01730; IWIQ.

DR HSSP; P01730; IWIQ.

GO: GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR InterPro; IPR000973; CD4 TCAG.

DR InterPro; IPR003596; Ig_v.

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002805; 077593;

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Query Match
Best Local Similarity
Matches 147; Conserv
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SMART; SM00406; IGv; 1.
Immunoglobulin domain; Transmembrane; Glycoprotein; T-cell;
Lipoprotein; Palmitate; Repeat.
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Harris E.E., Disotell T.R.;
"Nuclear gene trees and the phylogenetic relationships of the mangabeys (Primates: Papionini).";
Mol. Biol. Evol. 15.892-900 (1998).
-i- FUNCTION: ACCESSORY PROTEIN FOR MHC CLASS-II ANTIGEN/T-CELL RECEPTOR INTERACTION. MAY REGULATE T-CELL ACTIVATION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

TISSUE-Peripheral blood;
TISSUE-Peripheral blood;
MEDILINE-98017879, PubMed=9379478;
Fomsgaard A., Mueller-Trutwin M.C., Diop O., Hansen J.,
Corbet S., Barre-Sinoussi F., Allan J.S.;
Corbet S., Barre-Sinoussi F., Allan J.S.;
Their respective simian immunodeficiency virus genes.";
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Eukaryota; Metazoa; Chordata; Craniat;
Mammalia; Eutheria; Primates; Catarrh
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NCBI_TaxID=9534;
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IG-LIKE C2-TYPE DOMAIN 2.
IG-LIKE C2-TYPE DOMAIN 3.
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CD4 (T-cell surface antigen
    Score 758; DB
Pred. No. 7.1e
l0; Mismatches
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                                                                                         DB 6;
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GO; GO:0016020; C:membrane; IEA.
GO; GO:0006955; P:immune response; I:
InterPro; IPR00973; CD4 TCAg.
InterPro; IPR003599; Ig.
InterPro; IPR003199; Ig-11ke.
InterPro; IPR00359; Ig_v.
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PRINTS; PR00692; CD4TCA
SMART; SM00409; IG; 3.
SMART; SM00406; IGV; 1.
Q8HZT7 PRELIMINARY,
Q8HZT7;
Q1-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=22174698; PubMed=12186836;
LaBonte J.A., Babcock G.J., Patel T., Sodroski J.;
"Blockade of HIV-1 Infection of New World Monkey Cells
Primarily at the Stage of Virus Entry.";
J. Exp. Med. 196:431-445 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lymphocyte antigen CD4.
Callithrix jacchus (Common marmoset).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8HZT8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PS50835; IG LIKE; 1.
457 AA; 50878 MW;
                                                                                                                                                                                                                                                                                                           LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                                                                                                                                                         QVFGLTVNPDTHLLQGQSLTLTLESPPGSSPSVECMSPRGKTIRGMKTLFMSQLEIQDSG
                                                                                                                                                                                                                                                                                                                                                                                               ILGNQGSFLTKGPSKLNDRADSRRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
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                                                                                                                                                                           TWKCTVSQHLELV-FKINIV
                                                                                                                                                                                                                      TWTCTVLQNQKKVEFKIDIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VVLGKKGDTVELTCNASOKTTTOFHWKNSNOTKILGKOGSFLTKGSSKLRDRIDSRKSLW
                                                                                                                                                                                                                                                                                                                                                                      ILGIQGSFVTKGQSKLANRIDSKQSSWDRGSFPLIIRNVQVEDSETYICEVESKKEEVEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MNGGIPFRHSLLVLQLALLIAVTHGKTVVLGKKGEMVELPCETSLKKKLQFHWKTSNQIK
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                                                   PRELIMINARY;
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72.5%;
  23,
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Pred. No. 2.4e
23; Mismatches
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QSYSTA

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DT 01-NO

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DE T-cell

OS Delpho

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Best Local Similarity
Matches 144; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00047; ig; 2.
Pfam; PF00047; ig; 2.
PRINTS; PR00692; CD4TCANTIGEN.
SMART; SM00409; IG; 3.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
SECUENCE 457 AA; 50899 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9XS78;
Q9XS78;
01-NOV-1999
                                                         TISSUE=Thymus;

MEDLINE=99216435; PubMed=10199913;

Romano T.A., Ridgway S.H., Felten D.L.,

"Molecular cloning and characterization
the white whale Delphinapterus leucas.";

Immunogenetics 49:376-383(1999).
                                                                                                                                                                                                                                                                                01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
T-cell surface glycoprotein CD4.
Delphinapterus leucas (Beluga whale).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel
Mammalla; Eutheria; Cetartiodactyla; Cetacea; Odontoceti;
Monodontidae; Delphinapterus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2003 (TrEMBLrel. 23, Last & 01-OCT-2003 (TrEMBLrel. 25, Last & Lymphocyte antigen CD4. Saimiri sciureus (Common squirrel Saimiri sciureus)
  EMBL; AF071799; AAD23738.1;
HSSP; P01730; 1WIQ.
GO; GO:0016020; C:membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Exp. Med. 196:431-445(2002).

EMBL; AF452617; AAN14533.1; -.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0006955; P:immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Platyrrhini; Cebidae;
                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                            NCBI_TaxID=9749;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000973; CD4 TCAG.
InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Primarily at the Stage of Virus Entry.";
J. Exp. Med. 196:431-445(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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72.0%;
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    IEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 740.5;
Pred. No. 2.9e
24; Mismatches
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annotation update)
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World Monke
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of CD4 in
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Monkey
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Cebinae; Saimiri.
                                                                                                                      aquatic
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                                                                                                                      mammal,
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RESULT 11
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                                                                                                                             SETTER BURKER BREEF TO BE SEE TO BE SEED TO BE SE
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Best Local :
Query Match
Best Local Similarity
Matches 121; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0006955; P:immune response; IEA.
InterPro; IPR000973; CD4 TCAG.
InterPro; IPR007110; Ig-Tike.
InterPro; IPR007156; Ig_v.
Pfam; PF00047; ig; 3.
PRINTS; PR00692; CD4TCANTIGEN.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 2.
SEQUENCE 455 AA; 50499 MW; AA532FD441
                                                                                                                                                                                                                                                                                                                                                      the V-like region.";
Immunology 75:74-79(1992).
EMBL; AB000483; BAA19124.1; -.
HSSP; P01730; 1WIQ.
GO; GO:0016920; C:membrane; IEA.
GO; GO:0006955; P:immune response; IE
InterPro; IPR000973; CD4 TCAg.
InterPro; IPR007110; Ig-Tike.
InterPro; IPR007596; Ig-V.
                                                                                                                                                                                   Signal.
SIGNAL
                                                                                                                          CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CD4 antigen precursor.
Felis silvestris catus (Cat).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P79355;
01-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Miyazawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-1997
                                                                                                                                                                                                                                              PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
Miyazawa T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P79355
                                                                                                                                                                                                                                                                                                                                          Pfam; PF00047;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Norimine J., Miyazawa T., Kawagu
"A cDNA encoding feline CD4 has
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=92165316; PubMed=1537604;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -OCT-2003
                                                                                                                                                                                                                     Provided Reserved Res
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QVFRLTASSDTRLLLGQSLTLTLEGPSGSNPSVQWKGPGNKRKNEAKSLSLPQVGLQDSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TWTCTVSQAQQTLVFNKHIL
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474
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42.3%;
nilarity 55.3%;
Conservative 30
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                                                                                                                                                                                                                                                                              ; 1g; 3.
92; CD4TCANTIGEN.
                                                                                                                             Ā,
                                                                                                                             52243 MW;
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         30;
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Pred. No. 2.7e-43;
                                                                                                                                                      POTENTIAL.
   Score 557.5; DB
Pred. No. 3e-40;
0; Mismatches
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                                                                                                                          D946DD4BEAED00EC
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         49;
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                                                              474;
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downstream
      19;
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Best Local S
Matches 103
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EMBL; M17080; AAA37402.1; JOINED.

EMBL; M17076; AAA37402.1; JOINED.

EMBL; M17077; AAA37402.1; JOINED.

EMBL; M17078; AAA37402.1; JOINED.

EMBL; M17079; AAA37402.1; JOINED.

EMBL; M17079; AAA37402.1; JOINED.

HSSP; P01730; IMBR.
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Q61396;
Q61396;
Q61-NOV-1996
Q1-NOV-1996
Q1-OCT-2003
                                                                                                                                                                                                                                                                                        MGD; MGI:88335; Cd4.
GG; GO:0016020; C:membrane; IEA.
GG; GO:0006955; P:immune response;
InterPro; IPR000973; CD4 TCAg.
InterPro; IPR007110; Ig-Tike.
InterPro; IPR003596; Ig_v.
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Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
SEQUENCE 457 AA; 51368 MW;
                                                                                                                                                                                                                                                        Pfam; PF00047; ig; 2.
PRINTS; PR00692; CD4TCANTIGEN.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                brain."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=88041159; PubMed=2823269; Gorman S.D., Tourvieille B., Parn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T-cell differentiation antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Structure of the mouse gene encoding
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 176
                                                                                                                                                                             tch 35.5%; al Similarity 52.3%; 103; Conservative 3
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LQDSGTWTCTVLQNQKK 192
                                      EVOLLVFGLTANSDTHLLQGQSLTLTLES-PPGSSPSVQCRSPRGKNIQGGKTLSVSQLE 175
                                                                                          KILGNQG-SFLTKG--PSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKE
                                                                                                                             MCRAISLRRLLLLLQLSQLLAVTQEKTLVLGKEGESAELPCESSQKKITVFTWKFSDQR
                                                                                                                                        MNRGVPFRH-LLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ELLVFGLTAKVDPSGSGGSSSSSSTSTSTSIYLLQGQSLTLTLESPSSSNPSVQWKGPGNK
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                         EVELWVFKVTFSPGTSLLQGQSLTLTLDSNSKVSNPLTECKHKKGKVVSGSKVLSMSNLR 179
                                                                            KILGOHGKGVLIRGGSPSOF-DRFDSKKGAWEKGSFPLIINKLKMEDSOTYICELENRKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 (TrEMBLrel. 01,
5 (TrEMBLrel. 01,
3 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chordata;
Rodentia;
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Last seq
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                                                                                                                                                                             Score 467; DB 11;
Pred. No. 2.3e-32;
2; Mismatches 56;
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Best Local S
Matches 92
                                                                           O77596;
01-NOV-1998 (TrEMBLrel. 08, C:
01-NOV-1998 (TrEMBLrel. 08, L:
01-OCT-2003 (TrEMBLrel. 25, L.
T-cell surface glycoprotein C
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GO; GO:0016020; C:membrane; IEA.
GO; GO:0006955; P:immune response;
InterPro; IPR000973; CD4 TCAg.
InterPro; IPR007110; Ig-Tike.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Maddon P.J., Molineaux S.M., Alt F.W., Chess L., Axel R.; Submitted (FEB-1998) to the E EMBL; AF045882; AAC01764.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sec
01-JUN-1998 (TrEMBLrel. 25, Last an)
T4 surface glycoprotein (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00047; ig; 2. PRINTS; PR00692; CD47 SMART; SM00406; IGv;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=88097446; PubMed=3501122; Maddon P.J., Molineaux S.M., Maddon Matter R.; Maddon Axel R.; Maddon R.; Matter R.; Ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               055054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Structure and expression of the human and mouse Proc. Natl. Acad. Sci. U.S.A. 84:9155-9159(1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 141
                                                                                                                                                                                                                                                                                                                                                                                                                                       120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P01730; 1WBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     l Similarity
92; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLT 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PS50835; IG_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LTLES-PPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DSKKGAWEKGSFPLIINKLKMEDSQTYICELENRKEEVELWVFKVTFSPGTSLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QKTLVLGKEGESAELPCESSQKKITVFTWKFSDQRKILGQHGKGVLIRGGSPSQF-DRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQG-SFLTKG--PSKLNDRA
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                                                                                                                                                                                                                                                                                                                                                                                                                                LTLDSNSKVSNPLTECKHKKGKVVSGSKVLSMSNLRVQDSDFWNCTVTLDQKK
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sphinx (Mandrill)
Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    433 AA;
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                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CD4TCANTIGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48590 MW;
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Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29;
                                                                                            Created)
Last sequence update)
Last annotation update)
CD4 (T-cell surface ant
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 436.5; DB 1
Pred. No. 9.9e-30;
9; Mismatches 47
(Papio sphinx)
Craniata; Ver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Maddon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AB19330750A8499A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D.E.,
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Vertebrata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47;
                                                                                                antigen
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   Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        К. A.,
                                                                                                T4/LEU-3)
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                                                                                                                                                                                                                                                                                                                                                   RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 76
                                                                                  MEDLINE=98320077, ...
Harris E.E., Disotell T.R.;
Whuclear gene trees and the phylogenetic mangabeys (primates: Papionini).";
Mol. Biol. Evol. 15:892-900(1998).
-i- FUNCTION: ACCESSORY PROTEIN FOR MHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunoglobulin on TER 1
DOMAIN 1
DOMAIN 20
EMBL; AF057387; AAC25131.1;
HSSP; P01730; 1CDY.
GO; GO:0016021; C:integral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ONE V-LIKE AND 1 C2-LIKE D
EMBL; AF057386; AAC25130.1; -.
HSSP; P01730; 1CDY.
                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=98320644; PubMed=9656488;
Harris E.E., Disotell T.R.;
                                                                                                                                                                                            Cercopithecinae;
NCBI_TaxID=9568;
                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                         (Fragment).
Mandrillus leucophaeus (Drill) (Papio leucophaeus)
                                                                                                                                                                                                                                                                  T-cell surface
                                                                                                                                                                                                                                                                                         01-NOV-1998
                                                                                                                                                                                                                                                                                                                            077597
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cercopithecinae; Mandrillus.
NCBI_TaxID=9561;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mangabeys (primates: Papionini).";
Mol. Biol. Evol. 15:892-900(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Harris E.E., Disotell T.R.;
"Nuclear gene trees and the phylogenetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nterPro;
                                 SUBUNIT: ASSOCIATES WITH P56-LCK (BY SIMILARITY).
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMIL
SIMILARITY: BELONGS TO THE INMUNOGLOBULIN SUPERFAMILY.
ONE V-LIKE AND 1 C2-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: ASSOCIATES WITH P56-LCK (BY SIMILARITY).
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
SIMILARITY: BELONGS TO THE IMMUNOCLOBULIN SUPERFAMILY. CONTAINS
ONE V-LIKE AND 1 C2-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: ACCESSORY PROTEIN FOR MHC RECEPTOR INTERACTION. MAY REGULATE 1
                                                                                 SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO:0016021;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       107
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                                                                                                                                                                                                                                                                                                                                                                                   RTLSVPQLERQDSGTWTCTVSQDQK
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8 (TrEMBLrel. 08, 1
3 (TrEMBLrel. 25, 1
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20
49
86
8A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C:integral
                                                                                                                                                                                                           Mandrillus.
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78
78
86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T-cell; MHC; Transmembrane
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ç
                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
CD4 (T-cell surface antigen
                                                                                                                                                                                                                                                                                                    Created)
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Pred. No. 1.9e
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IG-LIKE V-TYPE DOMAIN.
IG-LIKE C2-TYPE DOMAIN
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2BD97A9EE19582AB CRC64;
  membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                   85
                                                                                                                                                                                                                                                                                                                            98
                                                                                           T-CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T-CELL ACTIVATION (BY
                                                                                                       CLASS-II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IEA
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.9e-27;
                                                                                                                                        relationships
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                                                                                                                                                                                                                                                                                       update)
                                                                                           -II ANTIGEN/T-CELL ACTIVATION (BY
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                                                          (BY SIMILARITY)
                                                                                                                                                                                                                                  Euteleostomi;
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                                                                                                                                                                                                                                                                   T4/LEU-3)
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RESULT 16
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Best Local
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Best Local
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NON TER 1
DOMĀIN <1
DOMAIN 20
DISULFID 49
NON TER 86
SEQÜENCE 86 AA
                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

MEDLINE-98320644; PubMed=9656488;

Harris E.E., Disotell T.R.;

"Nuclear gene trees and the phylogenetic relationships of the
"Nuclear gene trees and the phylogenetic relationships of the
mangabeys (primates: Papionini).";

MOI. Biol. Evol. 15:892-900(1998).

-I- FUNCTION: ACCESSORY PROTEIN FOR MHC CLASS-II ANTIGEN/T-CELL
RECEPTOR INTERACTION. MAY REGULATE T-CELL ACTIVATION (BY
                                                                                                                                                      DISULFID NON_TER
                                                                                                                                                                                                                                               -!- SUBUNIT: ASSOCIATES WITH P56-LCK (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMI)
-!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
ONE V-LIKE AND 1 C2-LIKE DOMAIN.
EMBL; AF057381; AAC25125.1; -.
HSSP; P01730; 1CDY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1998 (TrEMBLrel 08, 01-NOV-1998 (TrEMBLrel 08, 01-OCT-2003 (TrEMBLrel 25,
                                                                                                                                                                                        NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Cercopithe Cercopithecinae; Cercopithecus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           077594
                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=36225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cercopithecus mitis.
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                                                                                                                                          SEQUENCE
                                                                                                                                                                                                     Immunoglobul
NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            f-cell surface glycoprotein
                                                                                                                                                                             NIAMOC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Fragment)
                                                                                                                                                                                                                            nterPro;
                                                                                                                                                                                                               GO:0016021; C:integral to membrane; IEA. erPro; IPR007110; Ig-like. unoglobulin domain; T-cell; MHC; Transmen
                                                                                                                                                                                                                                                                                                                        SIMILARITY).
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                                                            YICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG
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RILSVPOLERODSGTWTCTVSQDQK
                      KILSVSQLELQDSGTWICTVLQNQK 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RTLSVPQLERQDSGTWTCTVSQDQK 85
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                                                                                                                                           9417 MW;
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Last sequence update)
Last annotation update)
CD4 (T-cell surface antigen
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Pred. No. 1
                                                                                                                                                               IG-LIKE V-TYPE DOMAIN.
IG-LIKE C2-TYPE DOMAIN
BY SIMILARITY.
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                                                                                                       Score 397; DB 6; Pred. No. 3.4e-27;
                                                                                                                                          371CA39EF58182AB CRC64;
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                                                                                            Mismatches
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                                                                                                                                                                             DOMAIN
                                                                                                                  Length 86;
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RESULT 17
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ID 07759
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Best Local S
Matches 75
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077599;
01-NOV-1998
01-NOV-1998
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01-NOV-1998
01-OCT-2003
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DOMAIN <1
DOMAIN 20
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NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -:- SUBUNIT: ASSOCIATES WITH P56-LCK (BY SIMILARITY).
-:- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
-:- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS ONE V-LIKE AND 1 C2-LIKE DOMAIN.
EMBL; AF057389; AAC25133.1; -
                                                                                                     Eukaryota; Metazoa; Chordata
Mammalia; Eutheria; Primates
Cercopithecinae; Cercocebus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP;
GO; G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIINE=98320644; PubMed=9656488;
Harris E.E., Disotell T.R.;
"Nuclear gene trees and the phylogenetic relation mangabeys (primates: Papionini).";
Mol. Biol. Evol. 15:892-900 (1998).
"Nol. Biol. Evol. 15:892-900 (1998).
"RECEPTOR INTERACTION. MAY REGULATE T-CELL ACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Theropithecus.
SEQUENCE FROM N.A.
MEDLINE=98320644; PubMed=9656488;
Harris E.E., Disotell T.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9565;
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                                                                                                                                                                         Cercocebus
                                                                                                                                                                                                                 T-cell surface
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                                                                               NCBI_TaxID=75569;
                                                                                                                                                                                         (Fragment).
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75; Conserv
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Metazoa; C
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                                                                                                                         us chrysogaster.
; Chordata; Cran:
; Primates; Cata
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88.2%;
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Last annotation update)
CD4 (T-cell surface antigen
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Last annotation update)
CD4 (T-cell surface antigen T4/LEU-3)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 397; DB 6;
Pred. No. 3.4e-27;
7; Mismatches 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IG-LIKE V-TYPE DOMAIN. IG-LIKE C2-TYPE DOMAIN. BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2BD97A98574EE9AB CRC64;
                                                                                                                             Craniata; Vertebrata; Euteleostomi; Catarrhini; Cercopithecidae;
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RESULT 19
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Best Local :
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                                                                                       EMBL; AF057388; AAC25132.1; --
HSSP; P01730; 1CDY.
GO; GO:0016021; C:integral to membrane;
InterPro; IPR007710; Ig-like.
Immunoglobulin domain; Glycoprotein; T-c
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DISULFID
NON_TER
                                                                                                                                                                                                                                                                                                                                     "Nuclear gene trees and the phylogenetic relationships of the mangabeys (primates: Papionini).";
Mol. Biol. Evol. 15:892-900(1998).
-I- FUNCTION: ACCESSORY PROTEIN FOR MHC CLASS-II ANTIGEN/T-CEI RECEPTOR INTERACTION. MAY REGULATE T-CELL ACTIVATION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1998 (TrEMBLrel. 08, 01-NOV-1998 (TrEMBLrel. 08, 01-OCT-2003 (TrEMBLrel. 25,
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MOI. Biol. Evol. 15:892-900(1998).

-!- FUNCTION: ACCESSORY PROTEIN FOR MHC CLASS-II ANTIGEN/T-CELL
RECEPTOR INTERACTION. MAY REGULATE T-CELL ACTIVATION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Papio.
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DOMĀIN
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                                                                           Immunoglobulin
NON_TER
                                                                                                                                                                                                                  -I- SUBUNIT: ASSOCIATES WITH P56-LCK (BY SIMILARITY).
-I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY)
-I- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAIL
ONE V-LIKE AND 1 C2-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98320644; PubMed=9656488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Papio sp. (Baboon).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Harris E.E., Disotell T.R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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SUBCELULIAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
SIMILARITY: BELONGS TO THE IMMUNOCLOBULIN SUPERPAMILY. CONTAIN
ONE V-LIKE AND 1 C2-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO:0016021; C:integral to membrane;
                                                                                                                                                                                                                                                                                                                   SIMILARITY)
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Last annotation update)
CD4 (T-cell surface antigen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
IG-LIKE V-TYPE DOMAIN.
IG-LIKE C2-TYPE DOMAIN.
N-LINKED (GLCNAC. . .)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 395; DB 6;
Pred. No. 5.1e-27;
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IG-LIKE C2-TYPE DOMAIN.
N-LINKED (GLCNAC. . .)
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                          MHC CLASS-II ANTIGEN/T-CELL ATE T-CELL ACTIVATION (BY
                                                                                            T-cell; MHC; Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98
                                                                                                                                              IEA.
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Best Local Similarity
Matches 74; Conser
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Best Local
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DOMĀIN <1
DOMAIN 20
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NON TER
SEQUENCE
                                                                                                                   DISULFID
NON TER
SEQUENCE
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01-NOV-1998 (TrEMBLrel. 08,
01-NOV-1998 (TrEMBLrel. 08,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                           Lophocebus albigena albigena.
Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Primates,
                                                                                                                                                                                                    <u>8</u>
                                                                                                                                                                                                                                                                                 mangabeys (primates: Papionini).";
Mol. Biol. Evol. 15:892-900(1998).
-I-FUNCTION: ACCESSORY PROTEIN FOR MHC
RECEPTOR INTERACTION. MAY REGULATE T
                                                                                                                                                                                                                                                                                                                                  MEDLINE=98320644; PubMed=9656488; Harris E.E., Disotell T.R.;
                                                                                                                                                                                                                                                                                                                                                                      Cercopithecinae;
NCBI_TaxID=75568;
                                                                                                                                                                                                                                                                                                                                                                                                                                    T-cell surface glycoprotein
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                                                                                                                                                                                                                                                                                                                        Harris E.E., Disotell T.R.; "Nuclear gene trees and the phylogenetic relationships
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                           (Fragment).
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                                                                                     Local
                                                                                                                                                                                         GO:0016021; C:integral to
erPro; IPR007110; Ig-like
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                                                                                                                                                                                                                                                                        SIMILARITY)
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RTLSVPQLERQDSGTWTCTVSQDQK
           KTLSVSQLELQDSGTWTCTVLQNQK
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86
7 AA;
                                                                             Conservative
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                                                                                                                                                                               domain;
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>86
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                                                                                                                    9463 MW;
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86
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87.1%;
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                                                                                                                                                                                T-cell; MHC; Transmembrane.
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Last annotation update)
CD4 (T-cell surface antigen T4/LEU-3)
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                                                                           Score 388; DB 6;
Pred. No. 2.1e-26;
7; Mismatches 4
                                                                                                                                      IG-LIKE V-TYPE DOMAIN IG-LIKE C2-TYPE DOMAIN BY SIMILARITY.
                                                                                                                    2BD97A88464FE9AB CRC64;
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Pred. No. 9.3e-27;
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                                                                                                                                                                                                   membrane;
                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Catarrhini; Cercopithecidae;
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T-CELL ACTIVATION
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Matches 73
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Q13969;
Q1-NOV-1996
Q1-JAN-1999
Q1-OCT-2003
            SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A., Nedospasov S.A.;
Zverev V.V., Blinov V.M., Nedospasov S.A.;
"Splice-mediated insertion of antisence and sence Alu repeats
"Splice-mediated insertion of three exons of CD4 mRNA.";
CD4 gene: identification of three exons of CD4 mRNA.";
CD4 gene: identification of the EMBL/GenBank/DDBJ databases.
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NON TER
SEQUENCE
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DOMAIN <1
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                                                                                                            Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
Cercopithecinae; Lophocebus.
                                                                                                                                                       CD4 protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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Eukaryota; Metazoa; (
                                                                                                 NCBI_TaxID=9606;
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SEQUENCE FROM N.A.
MEDLINE=95407135; PubMed=7676667;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30; GO:0016021; C:integral to membrane; IEA
InterPro; IPR007110; Ig-like.
Immunoglobulin domain; Glycoprotein; T-cell
                                                                                                                                                                                                                                   22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: ASSOCIATES WITH P56-LCK (BY SIMILARITY).
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMIL
SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
ONE V-LIKE AND 1 C2-LIKE DOMAIN.
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73; Conserv
                                                                                                                                                                                                                                                                     RTLSVPQLERQDSGTWTCNVSQDQK
                                                                                                                                                                                                                                                                                     KTLSVSQLELQDSGTWTCTVLQNQK 191
                                                                                                                                                                                                                                                                                                                 YICEVEDKKEEVELLVFGLTANSDTHLLEGQSLTLTLESPPGTSPSVKCRSPRGKNIQVG
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                                                                                                                                                                  5 (TrEMBLrel. 01,
9 (TrEMBLrel. 09,
3 (TrEMBLrel. 25,
                                                                                                                                                        (Fragment).
                                                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                    (Human).
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Primates;
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Last sequence update)
Last annotation update)
CD4 (T-cell surface antigen
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Last
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IG-LIKE C2-TYPE DOI
N-LINKED (GLCNAC.
BY SIMILARITY.
                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                            Score 383; DB Pred. No. 5.7e 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                          A9D97A88464FE9BE
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                                                                                                             Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                               PRT;
                                                                                                                                                                   sequence update)
annotation update)
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5.7e-26;
5;
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                                                                                                              Euteleostomi; Homo.
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NFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTAN
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SFPLIIKNLEVTDSGIYICEVEDKRIEVQLLVFRLTAS

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RESULT
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NON TER 99 99
SEQUENCE 99 AA; 11170 xm.
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Q29027;
Q1-NOV-1996 (Tr
01-NOV-1996 (Tr
01-OCT-2003 (Tr
CD4, allele 1 )
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NON TER
SEQUENCE
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STRAIN=#1183; TISSUE=Blood;
STRAIN=#2183; TISSUE=Blood;
MEDLINE=93329116; PubMed=8335933;
MEDLINE=93329116; PubMed=8335933;
MEDLINE=93329116; PubMed=8335933;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; S79267; AAB35273.1; -. PIR; I60082; I60082. HSSP: pn1770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   receptor gene].";
Vopr. Virusol. 40:100-102(1995).
EMBL; X87579; CAA60883.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zverev V.V., Sidorov A.V., Nedospasov S.A., Udalova I.A., Andzhaparizde O.G., Blinov V.I" [Nucleotide sequence of two exons of the h
                                                                                                                                                                                                                                                                                                 EMBL; X65629; CAA4658
PIR; I47131; S21461.
HSSP; P01730; 1CDY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO; GO:0004872; F:receptor activity; InterPro; IPR007110; Ig-like. PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                   Pfam; PF00047; ig; 1.
SMART; SM00406; IGv;
                                                                                                                                                                                                                                                                                                                                                                               miniature.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP;
                                                                                                                                                                                                                                                       InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                    "Extensive allelic polymorphion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23
                                                                                                                                                                                                                                                                                                                                                            Immunol. 151:1365-1370(1993).
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                  32
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                                                                             Similarity
KKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFL-TKGPSKLNDRADSRRSLWDQG
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1 AA;
                                                                                                                                                                                                                                                                                                                                           CAA46583.1;
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7844 MW;
                                                                                                                                      11170 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chordata; Craniata; Ver
Cetartiodactyla; Suina;
                                                                           23.2%;
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98.6%;
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25,
                                                        16;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A5C9D84816135C86 CRC64;
                                                                           Score 305.5; DB
Pred. No. 4e-19;
                                                                                                                                        40BF080699CF5D0C CRC64;
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ina; Suidae;
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1.3e-24;
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                                                          Indels
                                                                                              Length
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Sus.
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Q90WB Q90WB AC Q90WB AC Q90WB DT 01-DE DT-Cel DE T-Cel CARCHO CO ARCHO CO ARCHO CO NCEL RN [1] RN [1] RN [1] RA CHARL SUBMIL RA CHARL SUBMIL RA CHARL SUBMIL RA CHARL SUBMIL RA 
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                      Signal.
                                                                                                                                                                  TISSUE-Spleen;
Chan S.W.S., Middleton D.L.,
Submitted (MAY-2001) to the
EMBL; AF378701; AAKS9279.1;
                                                                                                                                                                                                                                                                                                                      Anas platyrhynchos (Domestic duck).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleos
Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
T-cell surface glycoprotein CD4 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      290WB5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50815; IG-LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-93329116; PubMed-8335933; Gustafsson K., Germana S., Sundt T "Extensive allelic polymorphion in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2003 (TrEMBLrel. 0
01-OCT-2003 (TrEMBLrel. 2
CD4, allele 2 (Fragment).
                                                        Pfam; PF00047; ig; 4.

SMART; SM00409; IG; 3.

PROSITE; PS50835; IG_LIKE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X65630; CAA46584.1; -. PIR; I47132; S21462. HSSP; P01730; 1CDY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=#1183; TISSUE=Blood;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q29028;
01-NOV-1996
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  SEQUENCE
                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                  NCBI_TaxID=8839;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQÜENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9823;
[1]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996
                                                                                                                         InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
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  482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99 AA;
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ilarity 56.1%;
Conservative 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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29 E
54624 MW;
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25,
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                                                                                                                                                                                             Lundqvist M., Warr G.W., H
EMBL/GenBank/DDBJ databases
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Pred. No. 6.2e
9; Mismatches
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POTENTIAL.
BDA0E8EC6172AD0B
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  CRC64;
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                                                                                                                                                                                                                                                                                                                                               Euteleostomi;
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Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ö.
                                                                                                                                                                                                               Higgins
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                                                                                                                                                                                                                 D.A.;
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Q2912

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Query Match
Best Local Similarity
Matches 50; Conserv
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Best Local
                                                                                                                                                                           InterPro; IPR007110; Ig-līke.
InterPro; IPR003598; Ig c2.
InterPro; IPR003999; VCAM-1.
Pfam; PF00047; 1g; 5.
PRINTS; PR01472; ICAMVCAM1.
PRINTS; PR01474; VCAM1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q29123
Q29123;
                                                                                         Immunoglobulin
SEQUENCE 538
                                                                                                                                   SMART; SM00408; IGC2; 3.
PROSITE; PS50835; IG_LIKE; 4.
                                                                                                                                                                                                                                                                                                                                        GO; GO:0016020; C:membrane; GO; GO:0016337; P:cell-cell
                                                                                                                                                                                                                                                                                                                                                                                    EMBL; L43124; AAB59281.1;
HSSP; P19320; IVCA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mueller J.P., Evans Elliott E.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=96106491; PubMed=8525525;
Mueller J.P., Evans M.J., Cofiell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vascular cell adhesion molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996
                                                                                                                                                                                                                                                                                           InterPro; IPR003987; ICAM VCAM-1.
InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Transplantation 60:1299-1306(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      specific for porcine VCAM.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cell adhesion to human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biochem. Biophys. Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tsang Y.T., Haskard D.O., Robinson M.K.; "Cloning and expression kinetics of porcine vascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=94271236; PubMed=7516159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sus scrofa (Pig)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Porcine vascular cell adhesion molecule (VCAM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           œ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LVFGLTANSDTHLLQGQSLTLT-LESPPGSSPS------VQCRSPRGKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RAVFVLLQLGL--THIMAHQQQIGVEGKEVILNC---KKHDKDVTWKYEYDAGSSAIIIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWK-----NSNQIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IQGGKTLSVSQLELQDSGTWTCTVLQN----QKKVEFKIDIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HVVKLTISSNGYFLPGDDLELTVMHKSPKSQPRFSITLFNSHNSRVTPEVLQNETPQ---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TremBLrel. 01, Created)
(TremBLrel. 01, Last sequence up
(TremBLrel. 25, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KYALKVKQLQPTDSGTWICNMHSDSPSINENISFNVKVL
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  Conservative
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                                                                                                                domain
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                                                                                         58713 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13.1%;
25.7%;
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25.0%;
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  38;
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                                                                                                                                                                                                                                                                                                                                        IEA.
adhesion;
Score 157.5;
Pred. No. 3.2e
38; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 1.5e
1; Mismatches
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Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                         8A7CD36D0A2F0717 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                201:805-812(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Development of blocking antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ₽.
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                                                                                                                                                                                                                                                                                                                                             IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rother R.P., Matis
3.2e-05;
nes 71;
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                                            DB
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                                          6;
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  Indels
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Sus.
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  41;
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003598; Ig c2.
InterPro; IPR003989; VCAM-1.
Pfam; PF00047; ig; 5.
PRINTS; PR01472.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00408; IGC2; 3.
PROSITE; PS50835; IG LIKE; 4.
Immunoglobulin domain; Signal.
SIGNAL 1 24 P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sus scrofa (Pig).
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-94271236; PubMed=7516159;
Tsang Y.T., Haskard D.O., Robinson M.K.;
"Cloning and expression kinetics of porc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01.NOV-1996 (TrEMBLrel. 01, Created)
01.NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Vascular cell adhesion molecule precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR01472; ICAMVCAM1.
PRINTS; PR01474; VCAM1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0016020; C:membrane; IEA. GO; GO:0016337; P:cell-cell adhes InterPro; IPR003987; ICAM_VCAM-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U08351; AAA215, PIR; JC2457; JC2457.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biochem. Biophys. Res. Commun. EMBL; U08351; AAA21542.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           molecule."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Aorta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q28939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP; P19320; 1VCA.
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                                                                                                                                                                                                                                                                                                                                                                                       Similarity
EFKIDIVPRASALPAPPTGS
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                                                              TCSSDGFPAPKILWSKKLRDGNLEPLSENTTLTLTSTKMEDSGIYVCEGINQAGINRKEV
                                                                                                                                                                ATLTLIAMRMEDSGIYVCEGVNPVGTNRKEVELTVQVAPRDTTISVNPSSTLEEGSSVNM
                                                                                                                                                                                                                                                                                                               KKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGN
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                                                                                                            TLESPPGSSPSV----QCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQ----NQKKV
                                                                                                                                                                                                            FPLIKNLKIEDSDTYICE----VEDQKEEVQLLV-----FGLTANSDTHLLQGQSLTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                             25
538 AA;
                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                538 V.
58795 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chordata; Craniata; Vertebrata;
Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                     11.9%;
                                                                                                                                                                                                                                                                                                                                                                39;
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                                                                                                                                                                                                                                                                                                                                                           Score 156.5; DB 6;
Pred. No. 3.9e-05;
9; Mismatches 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
VASCULAR CELL ADHESION MOLECULE.
; EC29D11B224F7261 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          411
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                                                                                                                                                                                                                                                              -SKKLDNGDQQLL---SGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Euteleostomi;
Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cell
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                                                              391
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RESULT
Q9D7B8
ID Q9
AC Q9
DT 01
DT 01
DT 01
DT 21
DT 21
DT 21
DT 01
DT 0
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Best Local S
Matches 59
                                                                                                                   Q9D7B8
Q9D7B8;
Q9D7B8;
01-JUN-2001
01-JUN-2001
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1999
01-NOV-1999
01-OCT-2003
CD4 protein
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SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9W6V7;
                             2310016B05Rik protein.
D11ERTD736E OR 2310016B05RIK.
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Koskinen R.H., Salomonsen J., Tregaskes C.A., Goodchild M., Bumstead N., Vainio O.; "The chicken CD4 general remained conserved i Immunogenetics 0:0-0(2002).

EMBL; Y12012; CAA72740.1; -.

EMBL; AJ401223; CAC82027.1; -.
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Gallus gallus (Chicken).
General Chordata;
   Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam;
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MEDLINE=99218434; PubMed=10201936;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Archosauria; Aves; Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=B12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vainio O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Koskinen R., Lamminmaki U.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Cloning and modeling of the first J. Immunol. 162:4115-4121(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28
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                                                                                                                                                                                                                                                                                                                                                                                                                     183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 NQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 VILVLQLGLTPIMAQQEQQI-GIAGKEVILSCKAINNQKDGTCTWKYKYKEVSSTIISFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 LLLVLQLALLPAATQGNKVVLGKKGDTVELTCTA-SQKKSIQFHWKN-----SNQIKILG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GKTLSVSQLELQDSGTWTCTVLQNQKKVEFKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KLTISSNGHFLTNEDLELTLMQNSSHSQPHLSIKLFNINNDIVTTEILQEEAPQ-KYI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLTANSDTHLLQGQSLTLTL-ESPPGSSPS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KAQVFKGKAPM-----THRSELNSNSKKLKVSDLSLDDAGIYTCACYSPVVSISLHVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PS50835;
   Metazoa;
                                                                                                                      (TrEMBLrel. 17, 17) (TrEMBLrel. 17, 17) (TrEMBLrel. 25, 17)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          487
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                                                                                                                                                                                                                                                                                                                                                                                                                  LKLKQLKAIDSGTWMCHVYSNSPSINQNI
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                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; 3.
IG_LIKE;
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54985 MW;
Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.6%;
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                                                                                                                          Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 153;
Pred. No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi;
; Galliformes; Phasianidae; Phasianinae;
Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           411
                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B9CBA92EC9F7F45B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nonmammalian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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Q9GKR2
ID Q9GKR
ID Q9GKR
AC Q9GKR
AC Q9GKR
DT 01-MA
DT 01-MA
DT 01-MA
DT 01-MA
COLUMN 
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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kasukawa T., Saito R.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Sakamoto N.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Hynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hynshakaki Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 68
                                                                                                                                                                                                                                                                                                                                                                                                Q9GKR2
Q9GKR2;
Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora;
                                                                                                                                                                                                                      01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Vascular cell adhesion molecule-1 6D variant lack
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SMART; SM00409; IG; 1.
PROSITE; PS50835; IG LIKE; 1.
SEQUENCE 287 AA; 32061 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Functional annotation of a full-length mouse Nature 409:685-690(2001).
EMBL, AK009375; BAB26251.1;
                                                                                                                                                precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=21085660; PubMed=11
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InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGD; MGI:1289168; D11Ertd736e.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RPLVLLWGCLVLPGYEALKGPKEISGFEGDTVSLRCTYVEKMKEHRKYWCRQGGILVSRC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ------SALPAPPT----GSALPDPQTASALPD-----PPAASALPAALAVISFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SLLLAAGLIAFGSHMLRWRKKAWLATETQKNEKVYLETSLPGNGWTTEDSTIDLAVTPEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFK-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---ILGNOGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVE----D
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                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 144; DB
Pred. No. 0.000
46; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSP----R
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).00021;
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                                                                                                                                                                                                                          update)
It lacking
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                                                    Euteleostomi;
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                 Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----IDIVPRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72;
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RESULT
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Best Local S
Matches 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AB052747; BAB19782.1; --
HSSP; P19320; 1VCA.
InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig_c2.
Pfam; PF00047; ig; 6.
SMART; SM00408; IGc2; 2.
SMART; SM00408; IGc2; 2.
InterPro;
InterPro;
Pfam; PF00
                                                                                                                                                                                                                                01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation updat
Vascular cell adhesion molecule-1 7D variant prec
                                                                                                                                                                                                                                                                                          Q9GKR3
                                                                                                                STRAIN-Holstein; TISSUE-Musc
Muroya S., Nakajima I., Chik
"Novel alternative splicing
                                                    88
                                                                        EMBL; AB052746; BAB19650.1; HSSP; P19320; IVCA.
                                                                                              Submitted
                                                                                                                                                   SEQUENCE
                                                                                                                                                                      NCBI_TaxID=9913;
                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Crania
Mammalia; Eutheria; Cetartiodactyla;
Bovidae; Bovinae; Bos
                                                                                                                                                                                                                 Bos taurus (Bovine).
                                                                                                                                                                                                                           Vascular cell adhesion VCAM1.
                                                                                                                                                                                                                                                                     Q9GKR3;
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Holstein; TIS
Muroya S., Nakajima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9913;
                                                                                                         molecu.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           molecule-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Nove]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bovidae;
                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mmunoglobulin domain; Signal
                                                                                                                                                                                                                                                                                                                31
                            GO:0016020; C:membrane; IEA.
GO:0016337; P:cell-cell adhes
erPro; IPR003987; ICAM VCAM-1.
erPro; IPR007110; Ig-11ke.
                                                                                                                                                                                                                                                                                                                                                388
                                                                                                                                                                                                                                                                                                                                                                                           328
                                                                                                                                                                                                                                                                                                                                                                                                              136
                                                                                                                                                                                                                                                                                                                                                                    188
                                                                                                                                                                                                                                                                                                                                                                                                                                   268
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                                                                                                       le-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
; IPR003598; ; IPR003989; ; O0047; ig; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FROM
                                                                                                                                                 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                CGQKKLEKRIQVKP--YSFPSNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QEGDSVTMTCASAGLPAPRILWS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KKGDTVELTCTASOKKSIOFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bovinae;
                                                                                                                                                                                                                                                                                                                                                                    QNOKKVEFKIDIVPRASALPAPP
                                                                                                                                                                                                                                                                                                                                                                                           VGDSVVLTCDVRDCESPSFSWRTLIDSPLNGNVRSEGSKSTLTLSPVSFENEHFYLCTVM
                                                                                                                                                                                                                                                                                                                                                                                                                                   RQLLSENATLTLISMRAEDSGIYVCEGNNPVGKDRKEVKLTVQEKNFTVEISPGPQIAAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                       FPLIIKN------KKIEDSDTYICE----VEDQKEEVQLLV----FGLTANSDTHLLQ-
                                                                                                                                                                                                                                                                                                                                                                                                             -GQSLTLTLESPPGSSPSVQCR----SPRGKNI--QGGK-TLSVSQLELQDSGTWTCTVL
                                                                                               (DEC-2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  650
                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N.A.
in; TISSUE=Muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA;
                                                                                                                            TISSUE=Muscle;
ima I., Chikuni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       650
          ; Ig_c2.
; VCAM-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71821 MW;
                                                                                              to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 kuni K.;
variant of bovine vascular cell
                                                    adhesion;
                                                                                              EMBL/GenBank/DDBJ
                                                                                                                   variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 141; DB 6;
Pred. No. 0.0011;
5; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.

VASCULAR CELL ADHESION MO
VARIANT LACKING D7.

; 24244573EF2B5E40 CRC64;
                                                                                                                                                                                                      Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                           PRT;
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                                                                                                                                                                                                                                                                                                                                                408
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                                                                                                                                                                                             Ruminantia;
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                                                    IEA
                                                                                                                   bovine
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                                                                                                                                                                                                                                                 update)
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                                                                                                                                                                                                                                      precursor
                                                                                               databases
                                                                                                                    vascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
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                                                                                                                                                                                                       Euteleostomi;
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                                                                                                                                                                                             Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56;
                                                                                                                    adhesion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      adhesion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         135
                                                                                                                                                                                                                                                                                                                                                                                                              187
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RESULT
Q28260
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                                                                                                                                                                  SOUR REAL DESCRIPTION OF THE PROPERTY OF THE P
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                                                                     Query Match
Best Local S
Matches 47
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Best Local S
                                                                                                                                                                                                                                                                                              GO; GO:0016020; C:membrane; IBA.
GO; GO:0016337; P:cell-cell adhesion; II
InterPro; IPR003987; ICAM VCAM-1.
InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003989; VCAM-1.
Pfam; PF00047; ig; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PRO1472; ICAMVCAM1.
PRINTS; PRO1474; VCAM1.
SMART; SM000408; IGC2; 3.
PROSITE; PS50835; IG_LIKE; 5.
Immunoglobulin domain; Signal.
SIGNAL 1 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TrEMBLrel 01, Created)
01-NOV-1996 (TrEMBLrel 01, Last sequence update)
01-OCT-2003 (TrEMBLrel 25, Last annotation update)
Vascular cell adhesion molecule-1.
                                                                                                                                                               Immunoglobulin SEQUENCE 739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ballantyne C.M., Cl
Youker K.A., Smith
Willerson J.T.;
                                                                                                                                                                                                     PRINTS; PRO1472; ICAMVCAM1.
PRINTS; PRO1474; VCAM1.
SMART; SM00408; IGC2; 4.
SMARTS; PS50835; IG_LIKE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Increased Expression of VCAM-1 and ICAM-1 in Arteriopathy in the Dog.";
Submitted (JUL-1995) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Canis familiaris (Dog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q28260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32
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P19320; IVCA.
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52; Conserv
                                                                         Similarity
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KKGDTVELTCTASQKKSJQFHWK---NSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWD :: | : | : | : | : |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QNQKKVEFKIDIVPRASALPAPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              M N.A.
C.M., Clubb F.
Cmith C.W., F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  739 AA;
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                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                               domain.
AA; 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  739
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                                                                                                                                                                  81412 MW;
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                                                                                             10.0%;
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                                                                       35;
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Pred. No. 0.0013;
5; Mismatches 6
                                                                     Score 132; DB 6;
Pred. No. 0.0082;
5; Mismatches 6(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VASCULAR CELL ADHESION MOLECULE-1 VARIANT.
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                                                                                                                                                                  BB5DA3853739C615 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J.L., Radovencovic Hawkins H.K., Fra:
                                                                                                                                                                                                                                                                                                                                                                                                                       IEA
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                                                                       60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Early Cardiac
                                                                                                                Length 739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                     Indels
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Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Frazier
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                                                                     48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Allograft
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                                                                     Gaps
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RESULT
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Q92626;
01-FEB-1997 (TrEMBLrel. 02, 0
01-FEB-1997 (TrEMBLrel. 02, 1
01-OCT-2003 (TrEMBLrel. 25, 1
MYELOBLAST KIAA0230 (Fragmen)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FKU. .... SEQUENCE FKU. .... TISSUE-Bone marrow;

MEDLINE-97191544; PubMed=9039502;

MAGABE T., Seki N., Ishikawa K., Ohira

MAGABE T., Seki N., Miyajima N., Nom
         Pfam;
                        Pfam;
Pfam;
                                                                                                                                                                                                                             TISSUB=Melanoma;
Mitchell M.S., Kan-Mitchell J., Minev B., Edman C., Dear
Mitchell M.S., Kan-Mitchell J., Minev B., Edman C., Dear
"Identification of a novel melanoma gene (MC50) - likely
IL-1 receptor antagonist - which encodes epitopes recogn
Cytolytic T lymphocytes.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases
EMBL; D86983; BAA13219.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nagase T., Seki N., Ishikawa K., Ohira M., Kawarabayasi Y., Ohara Tanaka A., Kotani H., Miyajima N., Nomura N.; "Prediction of the coding sequences of unidentified human genes. The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced analysis of cDNA clones from cell line KG-1 and brain."; DNA Res. 3:321-329(1996).
                                                   InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                    "Assignment of a human chromosome 2p25.3 by fl
                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=95048383; PubMed=7959781; Weiler S.R., Taylor S.M., Deans R
                                                                                                                                                                          GO; GO:0005152; F:interleukin-1 red
GO; GO:0006955; P:immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
                                                                              InterPro;
                                                                                                          InterPro;
                                                                                                                     InterPro;
                                                                                                                                                                                                      HSSP;
                                                                                          nterPro;
                                                                                                                                                                                                                                                                                                                            EQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        237 QEGGSVTMTCASEGLPPPQIFWSKKLDNGNLQLL-----
                                                                                                                                                                                                        P05164;
                                                                                                                                                                                                                   AF200348;
                                                                           ); IPR002007; Anim peroxid
); IPR007110; Ig-like.
); IPR003598; Ig c2.
); IPR001611; LRR.
); IPR000483; LRR_Cterm.
); IPR000372; LRR_Nterm.
); IPR000379; LRR_typ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LTLTLESPPGSSPS----VQCRSPRG--KNIQGGK-TLSVSQLELQDSGTWTCTVLQNQK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SGNATLTLIAMRLEDSGTYVCEGVNEVGKDGKEVELIVQEKPFTVEISPGPQIIAQIGDS
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                                                   IPR002016;
IPR001007;
                                                                                                                                                                                                      1CXP.
        ig; 4.
LRR; 5.
                                   An_peroxidase;
                                                                                                                                                                                        F:interleukin-1 receptor antagonist activity; NAS
                                                                                                                                                                                                                   AAF06354.1; -.
                                                                                                                                                                                                                                                                                                                                                                  numan melanoma associated
by fluorescence in situ h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chordata;
Primates;
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                                                   Peroxidase.
                                                                                                                                             Anim peroxidase.
Ig-like.
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                           R.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1496
                                                                                                                                                                                                                                                                                                                                                                  situ hybridization.";
                                                                                                                                                                                                                                                                                                                                                                                                           Kan-Mitchell J., Mitchell
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                                                                                                                                                                                                                                                                       epitopes recognized
                                                                                                                                                                                                                                                                                      Edman C., Deans R. (MG50) - likely the
                                                                                                                                                                                                                                                                                                                                                                               gene MG50
                                                                                                                                                                                                                                                                                                                                                                                   (D2S448)
                                                                                                                                                                                                                                                                       gene for by human
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RESULT
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Best Local s
Matches 60
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SMART; SM00082; LRRCT; 1.

SMART; SM00013; LRRUT; 1.

SMART; SM00319; LRR TYP; 4.

SMART; SM00314; VWC; 1.

PROSITE; PS50134; VWC; 1.

PROSITE; PS501292; PEROXIDASE

PROSITE; PS01208; VWFC 1; 1.

PROSITE; PS50184; VWFC 2; 1.
                                                                                                                                                                                                                                        11)
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=22077705; PubMed=12082541;
De Juan C., Intesta P., Gonzalez-Que Juan C., Torres A.J.,
                                                                                                               Oncogene 21:3089-3094(2002).

- SIMILARITY: CONTAINS 1 MAM DOMAIN.
EMBL; AF478693; AAV77220 1; --
Genew; HGNC:19267; MDGA1.
GO; GO:0016163; Finitrogenase activity;
GO; GO:00016163; Pinitrogen fixation; IEA.
GO; GO:0009399; Pinitrogen fixation; IEA.
                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
61-YCOS-2003 (TrEMBLrel. 25, Last annotation update)
61-YCOS-2003 (TrEMBLrel. 25, Last annotation update)
61-YCOS-2003 (TrEMBLrel. 25, Last annotation update)
                                InterPro; IPR008957; FN_III-like.
InterPro; IPR003599; Ig.
InterPro; IPR0071110; Ig-like.
InterPro; IPR003598; Ig.c2.
InterPro; IPR000398; MAM_domain.
InterPro; IPR000318; Nitrognse_compl.
            Pfam; PF00047; ig;
Pfam; PF00629; MAM;
                                                                                                                                                                                                          "Genomic organization of a novel glycosy expressed in human tissues and tumors.";
                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q8NFP4
                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8NFP4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HATAFII -- VQALPQFTVTPQDRVVIEGQTVDFQCEAKGNPPPVIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EFKIDIVPRASALP---APPTGSALPDPQT----ASALPDPPAASA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ECSATGHPPPRISWTRGDRTPLPVDPRVNITPSGGLYIQNVVQGDSGEYACSATNNIDSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----TLESPPGSSPSVQCRSP----RGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LMIQNTQETDQGIYQCMAKNVAGEVKTQEVTLRYFGSPARPTFVIQPQNTEVLVGESVTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIIKNLKIEDSDTYICEV----EDQKEEVQLLVFGLTAN-----SDTHLLQGQSLTL
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                                                                                                                                                                                                                                     Benito M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VWC; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WC; 1.
; IG_LIKE; 4.
; PEROXIDASE 3; :
; VWFC_1; 1.
; VWFC_2; 1.
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MAMDOMAIN
                       6
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                                                                                                                                                                                                                                                Gonzalez-Quevedo R.,
rres A.J., Balibrea J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 131.5;
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                                                                                                                                                                                                                      glycosylphosphatidylinositol
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                                                                                                                  IEA.
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                                                                                                                              IEA
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                                                                                                                                                                                                                                                Moran A.,
.L., Diaz-Rubio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.
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                                                                                                                                                                                                                                                                                                                                           Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             232
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E
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                                                                                                                                                                                           Query Match
Best Local S
Matches 57
                                                                                                                                                                                                                                      Strauberg R.;
Strauberg R.;
Submitted (JUL-2002) to the EM
EMBL; BC033803; AAH33803.1; -.
InterPro; IPR003599; Ig. 1]:
InterPro; IPR003598; Ig-like.
InterPro; IPR003598; Ig_c2.
Pfam; PF00047; Ig; 3.
Pfam; PF00047; Ig; 3.
R SMART; SM00409; IG; 3.
R SMART; SM00408; IGc2; 3.
R PROSITE; PS50835; IG_LIKE; 3
R PROSITE; PS50835; IG_LIKE; 3
R SROUENCE 338 AA; 37393 MW
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Best Local S
Matches 48
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SMART; SM00408; IGC2; 6.
SMART; SM00137; MAM; 1.
PROSITE; PS50835; IG LIKE; 6.
PROSITE; PS50860; MAM 2; 1.
PROSITE; PS00609; NITROGENASE 1 1; 1.
Glycoprotein; Immunoglobulin domain.
SEQUENCE 955 AA; 105790 MW; BD41A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8IV49
Q8IV49;
01-MAR-2003
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR 2003 (TrEMBLrel 23, Created)
01-MAR-2003 (TrEMBLrel 23, Last sec
01-OCT-2003 (TrEMBLrel 25, Last and
Similar to limbic system-associated
                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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 182
                        169
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                                                                                                                                                                                                         Similarity
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                                                                                             -EVQLLVFG----LTANSDTHLLQGQSLTLTLESPPGSSPSVQCR--SPRGKNIQGGKT-
                                                                                                                                             LVLLRLLCLLPTGLPVRSVDFNRGTDNITVRQGDTAILRCVVEDKNS-KVAWLNRSGIIF
                                                                                                                                                               LLLVLQLALLPAA-----TQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KLKNLRPQDYASYTCQVSVRNVCGIPDKAITFRLTNTTAPPALK-LSVNETLVVNPGENV
                      LSVSQLELQDSGTWTCTVLQ----
                                                                                                                                                                                                                                                                                                                                                                                            FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SVQC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TVFLRCTVNSNPPARFIWKRGSD------TLSHSQDNG-VDIYEPLYTQGETKVL
LEILGITREQSGKYECKAANEVSSADVKQVKVTVNYPPTITESKSNEATTGRQASLKCEA
                                                SQVYLIVQVPPKISNISSDVTVNEGSNVTLVCMANGRPEPVITWRHLTPTGREFEGEEEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                - IKNIKIEDSDTYICEVEDQKE---EVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TVELTCTASOKKSIOFHWKNSNOIKILGNOGSFLTKGPSKLNDRADSRRSLWDQGNFPLI
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ilarity 27.3%;
Conservative 2
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Primates;
                                                                                                                                                                                                                                                                                                      ; Ig.
; Ig-like.
; Ig_c2.
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                                                                                                                                                                                           Score 130; DB 4;
Pred. No. 0.0044;
0; Mismatches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 131; DB 4
Pred. No. 0.014;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -RSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQN
                                                                                                                                                                                                                                             88CF00E07302817B CRC64;
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annotation update)
ted membrane protein.
                        -NOKKVEFKIDIVP--
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                                                                                                                                                                                                                    Length 338;
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RESULT 37
Q8IZFB
ID Q8IZF
AC Q8IZF
DT 01-MA
DT 01-MD
DT 01-OC
DE Necti
OS Homo
OC Bukar
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Best Local :
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GG); GO:0007411; P:axon guidance; IN
InterPro; IPR003961; FN III.
InterPro; IPR008957; FN III-like.
InterPro; IPR008957; FN III-like.
InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-like.
Pf6am; PF00041; fn3; 4.
Pfam; PF00047; ig; 6.
SMART; SM00408; IG2; 5.
SMART; SM00408; IG2; 5.
PROSITE; PS50835; IG_LIKE; 6.
Immnoglobulin domain.
                                                                    01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
01-OCT-2003 (TrEMBLrel. 25,
Nectin-like protein 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Comparative sequence analysis of the mouse Licam locus and corresponding region of human Xq28."; Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AF133.093; AAF22153.1; -. HSSP; P20241; ICFB.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                      Q8IZP8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9QY38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQ--FHWKNSNQIKILGNQGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLTAN-----SDTHLLQGQSLTLTLESPPGSSPSVQCRSP-----RGKNIQGGKTL 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----DLQERGDSDKYFIEDGK--LVIQSLDYSDQGNYSCVASTELDEVESRAQLLVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYIC----EVEDQKEEVQLLVF
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                                                                                                                                                                                                                                                                                                                                 SLGKV----
                                                                                                                                                                                                                                                                                                                                                                           SVSQLELQDSGTWTCTVLQNQKKVE--FKIDIVPRASALPAPPTGSALPDPQTA
                                                                                                                                                                                                                                                                                                                                                                                                                                  GSPGPVPHLELSDRHLLKQSQVHLSW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ILANLQVKEATQITQGPRSAIEKKGARVTFTCQASFDPSLQASITWRGDGR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel. 13, (TrEMBLrel. 25, )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1259 AA;
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                                                                                                                                                                                                                                                                                                                                 - PGNQTSTTLKLSPYVHYTFRVTAINKYGPGEPSPVSETVVTPEAA
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Last annotation
le L1.
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Last annotation update)
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Pred. No. 0.025;
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Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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  Euteleostomi; Homo.
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Best Local S
Matches 65
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Best Local S
Matches 57
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01-UUN-2002 (TrEMBLrel. 21
01-UUN-2002 (TrEMBLrel. 21
01-OCT-2003 (TrEMBLrel. 25
Polymeric immunoglobulin r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Piam; PF00047; ig; 3.

Piam; PF00047; ig; 2.

SMART; SM00409; IG; 2.

SMART; SM00408; IGc2; 3.

PROSITE; PS50835; IG_LIKE; 3.

PROSITE; PS50835; IG_LIKE; 3.
                                                                                               Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                        TISSUB=Mammary lymph node;
Taylor C.L., Harrison G.A.;
Taylor C.L., Harrison G.A.;
"cDNA cloning of the polymeric immunoglobulin
marsupial Macropus eugenii (tammar wallaby).";
Submitted (OCT-200) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gingrich J.R., D'Angelo A., Submitted (AUG-2002) to the EMBL, AP538973, AAN16368.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Macropus eugenii (Tammar wallaby).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleos
Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus
                                                                                                                                                                                                                                                          EMBL; AF317205; AAK69593.1; -. GO; GO:0004872; F:receptor activity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q8SPI6
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                                                                                                                                                                    Pfam; PF00047; ig; 5.
SMART; SM00409; IG; 5
                                                                                                                                                                                                              InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9315;
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                                                                                                                                              PROSITE; PS50835;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57;
  l Similarity
65; Conserv
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IPR007110; Ig-like.
IPR003598; Ig_c2.
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9.8%;
ilarity 23.6%;
Conservative 4
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Last
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EMBL/GenBank/DDBJ
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Pred. No. 0.0068;
  Score 129; DB 6;
Pred. No. 0.015;
7; Mismatches 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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annotation update)
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                                              Length 731;
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       64;
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Best Local S
Matches 56
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InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig_c2.
Pfam; PF00047; Ig; 3.
SMART; SM00409; IG; 3.
SMART; SM00409; IG; 3.
PROSITE; PS50835; IG_LIKE; 3.
SEQUENCE 341 AA; 38086 MW;
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01-MAR-2003 (TrEMBLrel 23
01-OCT-2003 (TrEMBLrel 25
Limbic system-associated m
B130007004RIK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8BLK3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N. STRAIN=C57BL/6J;
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MGD; MGI:2442078; B130007004Rik.
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The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the RIKEN Genome Exploration Research Group
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                                                                                                                                                                                                                                                                                                                                                               Similarity 56; Conserv
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LSVSQLELQDSGTWTCTVLQ-----NQKKVEFKIDIVP
                                                                                 SQVYLIVQVPPKISNISSDVTVNEGSNVTLVCMANGRPEPVITWRHLTPLGREFEGEEEY
                                                                                                                                                                                                                                                                                                            LLLVLQLALLPAA-----TQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QKEEVQLLVFGLTANSDTHLL---QGQSLTL--TLESPFGSSFSVQCR-------
                                                                                                                                                                          AGHD-----KWSLDPRVELEKRHAL----EYSLRIQKVDVYDEGSYTCSVQTQHEPKT
                                                                                                                                                                                                                      LGNQGSFLTKGPSKLNDRA--DSRRSLWDQGNFPLIJKNLKIEDSDTYICEVEDQKE---
                                                                                                                                                                                                                                                                      LVLLRLLCLLPTGLPVRSVDFNRGTDNITVRQGDTAILRCVVEDKNS-KVAWLNRSGIIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SKGFTNNSTHGRILFTPTEPGSFSIMITQVRKEDAGLYHCGAQENGEPSEKGPIQALQLF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----SPRGKNI-----QGGKTLSVSQLELQDSGTWTCTVLQNQKKVE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -FKIDIVPRASALPAPPTGSALP----
                                                                                                                                                                                                                                                                                                                                                            9.6%;
larity 22.8%;
Conservative 4
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                                                                                                                             LTANSDTHLLQGQSLTLTLESPPGSSPSVQCR--SPRGKNIQGGKT-
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23, Last s
25, Last a
d membrane |
                                                                                                                                                                                                                                                                                                                                                                 41;
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Last annotation update)
mbrane protein precursor
                                                                                                                                                                                                                                                                                                                                                            Score 126; DB
Pred. No. 0.009
41; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
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Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          949CE792C67E25C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -ERVRERISGTSSKVEVVIISQEKRQDVGTYICAVGED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        341
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on functional
                                                                                                                                                                                                                                                                                                                                                               91;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                     Length 341;
                                                                                                                                                                                                                                                                                                                                                                 Indels
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; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       annotation
                                                                                                                                                                                                                                                                                                                                                            58;
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Best Local S
                                                                                                                                                                                                                           Matches
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Q13857;
01-NOV-1996
01-NOV-1996
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Barnett T.R., Kretschwe...,
Elting J.J., Kamarck M.E.;
Elting J.J., Kamarck M.E.;
"Carcinoembryonic antigens: alternative splicing a
"ulliple mRNAs that code for novel members of the
antigen family.";
antigen family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biliary
BGP.
                                                                                                                                                                                                                                                                                                                                                                                 MEDIJINE-93140765; PubMed-8423792;
Barnett T.R., Drake L., Pickle W. II.;
"Human biliary glycoprotien gene: characterization novel alternatively spliced RNAs and their expresse Mol. Cell. Biol. 13:1273-1282(1993).

EMBL; M76741; AAA57141.1; -...
                                                                                                                                                                                                                                                                               Immunoglobulin
                                                                                                                                                                                                                                                                                                                                                            GO; GO:0005624; C:membrane fraction; GO; GO:0007565; P:pregnancy; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=89139550; PubMed=2537311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                      InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig_c2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40
                                                                                                                                                                                                                                                                                          n; PF00047; ig; i. TRT; SM00408; IGc2; 1.
SITE; PS50835; IG_LIKE; lunglobulin_domain.
 206
                      240
                                                                                       122
                                                                  180
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                                                                                                                                                                                                                                     Similarity
 VALVALIAVALACFL
                                                                                                                                                                                                   LLVLQLALLPAATQ----GNKVVLGKKGDTVELTCTASQKK-SIQFHWKNSNQIKILGNQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                    FROM N.A.
                                                                                                                                                                              IIVTELSPVVAKPQIKASKTTVTGDK
                                             NSWAQAIL
                                                                 GTWTCTVLQNQKKVEFKIDIVPRASALPAPPTGSALPDPQTASALPDPPAASALPAALAV
                                                                                        EMAF.
                                                                                                                                                         SFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEV-----EDQKEEVQL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ||:|||
SAVPAP 247
                     ISFLIGLGLGVACVL
                                                                                                            -LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDS
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                                                                                                                                    ----PS
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                                                                                                                                                                                                                                                                     226 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 25, Last annotation updat
                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chordata;
Primates;
                                                                                                                                                                                                                                     9.5%;
                                                                                                                                                                                                                                                                       24045 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Fragment).
                                                                                                                                    - SERMKLSOGNITLSINPVKREDAGTYWCEVFNPISKNOSDPIMLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01,
220
                      254
                                                                                                                                                                                                                           37;
                                                                                                                                                                                                                          Score 125.5; DB 4;
Pred. No. 0.0064;
7; Mismatches 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata;
Catarrhini; Hominidae;
                                            PSVSQ-SAEITDNALPQENGLS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                       8E11929059866970 CRC64;
                                                                                                                                                                              -DSVNLTCSTNDTGISIRWFFKNQSL--
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                                                                                                                                                                                                                                                                                                                                                                                                        rization of a family expressed proteins.
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e carcinoembryonic
                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Euteleostomi; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hart J.T.,
                                             PGAIAGI--VIGV
                                                                                                                                                                                                                           69;
                                                                                        -TMLPRLDS
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Of
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STARRED CORRES REPRESENTATION OF THE CONTRACT 
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Best Local S
Matches 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0004601; F:peroxidase activity; GO; GO:0006979; P:response to oxidative Interpro; IPR002007; Anim peroxidase. Interpro; IPR003599; Ig. Interpro; IPR003599; Ig. Interpro; IPR003598; Ig_cz. Interpro; IPR003598; Ig_cz. Interpro; IPR003596; Ig_v. Interpro; IPR003596; Ig_v. IPR001611; LRR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q80U60;
01-JUN-2003
01-JUN-2003
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Okazaki N., Kikuno R., Ohara R., Inamoto S., Aizawa H., Yuasa S., Nakajima D., Nagase T., Ohara O., Koga H.; "Prediction of the coding sequences of mouse homologues of KIAA ger II. The complete nucleotide sequences of 400 mouse KIAA-homologous cDNAs identified by screening of terminal sequences of cDNA clones randomly sampled from size-fractionated libraries.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                       SWART; SM00214; VWC; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS50292; PEROXIDASE_3;
PROSITE; PS01208; VWFC_1; 1.
PROSITE; PS50124; VWFC_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PRO0457; ANPEROXIDASE.
SMART; SM00409; IG; 4.
SMART; SM00408; IGC2; 4.
SMART; SM00406; IGC2; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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Pfam; PF00047; ig; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AK122223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=22579291;    PubMed=12693553;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [nterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO:0004601; F:peroxidase activity; IEA.
                                              142
                                                                                                                                                                                              213
313
                                                                                                                                             94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PF00560; LRR; 5.
PF01463; LRRCT; 1.
                                                                                                                                                                                                                                                                                              1 Similarity
57; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SM00214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; IPR003599; Ig-1ike.; IPR003598; Ig-2:; IPR003598; Ig-c2.; IPR003596; Ig-v.; IPR001611; LRR. Cterm.; IPR000483; LRR. Cterm.; IPR007992; LRR. SUS22.; IPR003591; LRR. Lyp.;
                                                                                                                                                                                                                                               GDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFP
                                              TLESPPGSSPSVQCRSPRGK----
                                                                                                                                           LIIKNLKIEDSDTYICEV-----EDQKEEVQLLVFGLTAN-----SDTHLLQGQSLTL 141
                                                                                                                                                                                                 GNTVYFTCRAEGNPKPEIIWLRNN-------NELSMKTDSRLNLLDDGT--
TLECSATGHPLPQITWTRGDRTPLPIDPRVNITPSGGLYIQNVAQSDSGEYTCFASNSVD
                                                                                            LMIQNTQEADEGVYQCMAKNVAGEAKTQEVTLRYLGSPARPTFVIQPQNTEVLVGES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPR001007;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR002016;
                                                                                                                                                                                                                                                                                                                                                                                                1431 AA; 160591 MW;
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(TrEMBLrel. 24, Last sequence up
(TrEMBLrel. 25, Last annotation
                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LRRCT; 1.
; LRR PS; 4.
; LRR TYP; 5.
; VWC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BAC65505.1; -.
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Rodentia;
                                                                                                                                                                                                                                                                                                                     9.5%;
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                                                                                                                                                                                                                                                                                                25;
                                                                                                                                                                                                                                                                                                                        Score 125.5;
Pred. No. 0.0
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                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                6BA952436DA54B72 CRC64;
                                                                                                                                                                                                                                                                                                                        No. 0.072;
                                           ----NIQGGKTLSVSQLELQDSGTWTCTVLQNQK
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                                                                                                                                                                                                                                                                                                                                               DB 11;
                                                                                                                                                                                                                                                                                                93;
                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                            Length
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                                                                                                                                                                                                                                                                                                                                                 1431;
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                                                                                               312
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RESULT RE
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Best Local S
Matches 68
                                                                                                                           Brachydanio rerio (Zebrafish)
Eukaryota; Metazoa; Chordata;
Actinopterygii; Neopterygii; T
                                                                                                                                                                                                                  Q8UV81 PRELIMINARY; PRT; 358 AA.
Q8UV81 (TrEMBLrel. 20, Created)
Q1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
Q1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
SC:GZ125733.3 (Novel immune-type receptor 1.10 (nitr1.10)).
SC:DZ125733.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PKUUUW;, -J.; 1.
SMART; SM00409; IG; 1.
PROSITE; PS50835; IG LIKE; 1.
PROSITE; PS50835; IG LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUDMITTED (MAR-2002) to the I
EMBL, BC025395; AAH25395.1; -
InterPro; IPR003599; Ig.
InterPro; IPR003110; Ig-like.
Pfam; PF00047: '--'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8TA95; PRELIMINARY;
Q8TA95; Q1-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.;
Submitted (MAR-2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similar to CMRF35 antigen precursor.
SEQUENCE FROM N.A Garner P.;
                                                                        NCBI_TaxID=7955;
                                                                                                          Cyprinidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Testis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KVEFKIDIVPRASALP---APPTGSALPDPQT----ASALPDPPAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSALPDPQ--TASALPDPPAASA------LPAALAVISFLLGLGLGVAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AQQTQPPGLTSPGLYPAATTAKQGKTGAEAPPLPGTSQYGHERTSQYTGTSPHPATSPPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LLI-----SLFVFPGPC-----CPPSPSPTFQ------PLATTRLQPKAK 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SGTIYAEEEGQETMKGRVSIRDSRQEL----SLIVTLWNLTLQDAGEYWCGVEKRGPDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QGSFLT--KGPSKLNDRA---DSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RLLVLLWGCLLLPGYEALEGPEEISGFEGDTVSLQCTYREELRDHRKYWCRKGGILFSRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RHLLLVLQLALLPA--ATOGNKVVLGKKGDTVELTCTASOK-KSIQFHWKNSNQIKILGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSSRPPMQLNSTSAEDTSPALSSGSSKPRVSIPMVRILAPVLVLLSLLSAAGLIAFC
                                                                                                             Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9.5%; Score 125; DB 4;
22.9%; Pred. No. 0.012;
live 38; Mismatches 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL/GenBank/DDBJ
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                                                                                                                                       ; Craniata;
Teleostei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                              (Danio rerio)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      159124621383CE93 CRC64;
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                                                                                                                                       Vertebrata; Euteleostomi;
Ostariophysi; Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           109;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 332,
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RESULT 44
Q9H1X9
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                                                       Query Match
Best Local
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Best Local
                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                             SEQUENCE Lawlor S.
                                                                                                                                                                                                                                                                                                                   01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation updat
BG15303.1 (Similar to C.elegans hemicentin) (Frag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00047; 19; 2.
SMART; SM00409; IG; 2.
PROSITE; PS50835; IG_LIKE;
                                                                                                    NON TER
                                                                                                                                                                                            Submitted (JUN-2000) to the EMBL; AL133515; CAC17584.1; HSSP; P56276; 1TLK.
                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata;
Mammalia, Eutheria, Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (DEC-2001) to the EMBL/GenBank/DDBJ EMBL, AL591405; CAD12581.1; -. GO; GO:0004872; F:receptor activity; IEA.
                                                                                                                        Pfam; PF00047; ig; 5.
SMART; SM00408; IGc2; 4.
PROSITE; PS50835; IG_LIKE;
Immunoglobulin domain.
                                                                                                                                                                                                                                                                                                           BG15303.1 (Similar
BG15303.1.
                                                                                                                                                                                                                                                                                                                                                                               Q9H1X9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
                                                                                         SEQÜENCE
                                                                                                                                                                   InterPro; IPR007110; Ig-like
InterPro; IPR003598; Ig_c2.
                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
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 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59;
                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
 GSNVTLPCYVQGYPEPTIKWRRLDNMPIFSR--PFSVSSISQLRTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                      ALLAL 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QGNKVVLGKKGDTVELTCTASQKKS1QFHW----KNSNQIKILGNQGSFLTKGP-----
                      GDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFP
                                                                                                                                                                                                                                        FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            RASAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPRGKNIQGGKT-----LSVSQLELQDSGTWTCTVLQ-----NOKKVEFKIDIVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SDTHLLQGQSLTLTLESPPGSSPSVQC------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EKMND----VNVIIEEGYFNLTILKTKPSDSATYYCIVSSYQAIGMGSGTRLIVRDAATD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQK----EEVQLLVFGLTAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QENNVKIVQAGEDVNLTCTFSPNMQLSTAWFKHTADGKTLQIVFN--LFFTKSPIWNNNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NGRCKNSAESETQSCVYSLHKNNISRSDTGIYYCAVAACGQILLGNGTQLNIRESGDLYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RNTTL--HQSLIDTVD--PGDSVNLQCSIFTESCAGDHNIYWFKQSSGDSEGVLYTKGER
                                                                                        390
390 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              358 AA;
                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            206
                                                                                                    390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40130 MW;
                                                                                         42153 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9.5%;
                                                      9.5%;
                                            26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29;
                                          Score 125; DB
Pred. No. 0.01:
26; Mismatches
                                                                                                                                                                                                                 EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 125;
Pred. No. 0.
                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                        E1F7B5D5BE6E19B4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BBAD75EBAEAB4953 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                               390
                                                      DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1
                                                                                                                                                                                                                                                                                                                                                                               ξ
                                                                                                                                                                                                                                                                                                                     update)
(Fragment)
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                                            92;
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                                                                                                                                                                                                                  databases
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                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                                            Indels
                                           56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72;
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                                          Gaps
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                      93
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225
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RESULT 46
Q9VCT4
ID Q9VCT
AC Q9VCT
DT 01-MA
DT 01-MA
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Q96DN8
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                                                                                                                                                                                                                                                                                         밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               096DN8;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein FLJ31774. Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                  LIIKNLKIEDSDTYICEVEDQ----KEEVQLLVFGLTA----NSDTHLLQGQSLTLTL
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                                                                                                                                                                                             NVAGTNNKTTSVVVHVLPTIQHGQQILSTIEGIPVTLPCKASGNPKP
                                                                                                                                                                                                                                          Q----NQKKVEFKIDIVP---RASALPAPPTGSALPDPQTASALPDP
                                                                                                                                                                                                                                                                                                                                         ESPPGS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GSNVTLPCYVQGYPEPTIKWRRLDNMPIFSR--PFSVSSISQLRTGA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NVAGTNNKTTSVVVHVLPTIQHGQQILSTIEGIPVTLPCKASGNPKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q----NQKKVEFKIDIVP---RASALPAPPTGSALPDPQTASALPDP
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                                                                                                                                                                                                                                                                                       TLLAGNPIPERRWIKNSAMLLQNPYITVRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.5%; Score 125; DB 4.
Larity 23.3%; Pred. No. 0.021;
Conservative 26; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                    -SPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVL
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                                                                                                                                                                                                                                                                                         -----DGSLHIERVQLQDGGEYTCVAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 512;
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; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8.,
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Q9VCT4 Q9VCT4; 01-MAY-2000 01-MAY-2000

(TrEMBLrel. (TrEMBLrel. PRELIMINARY;

Last Created)

sequence update)

545

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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams M.D., Celniker S.E., Holt R.A., Ashburner M.A., Galle R.F., Ra Amanatides P.G., Scherer S.E., Holt R.M., Hoskins R.A., Galle R.F., RA Amanatides P.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Phandon R.C., Miklos G.L.G., RA Barlis J.F., Apbayani A., An H.-J., Andrews-Frannkoch C.B., Miklos G.L.G., RA Barlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P., Rohadra I., RA Borkova D., Botcher A., Deng Z., Mays A.D., Dew I. Dietz S.M., Durbin K.G., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Fleischmann W., Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Goldek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris M.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., A Harris M.L., Mathan F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., A Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D. Lai Z., Liang Y., Lin X., Malskon P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Malskor P., Nelson D., Nelson M.V., Mobarry C., Morris J., Moshrefi A., RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Nelson D.M., Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., Ra Nelson D.R., Nelson K.A., Nixon K., Skupski M.P., Smith T., RA Palzer B., C., Staplecon M., Stupski M.P., Smith T., Ra Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Smith H.O., Zheng Y., Yen R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Z
                                                                                                                                                                                            Gonzalez M., Ghavez C., Dorsett V., Farfan D., Frise E., George R., Gunzalez M., Guarin H., Li P., Liao G., Miranda A., Mugall C.J., Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K. Yu C., Lewis S.E., Rubin G.M., Celniker S.; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AE00374; AAF56071.1; -. EMBL; AY060363; AAL25402.1; -. EMBL; Pagn0017590; klo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                   FlyBase; FBgn0017590; klg.
InterPro; IRR003961; FN III.
InterPro; IRR008957; FN III-like.
InterPro; IRR007110; Ig-like.
InterPro; IRR003598; Ig_c2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=20196006; PubMed=10731132;
Immunoglobulin
SEQUENCE 545
                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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OR CG6669
                                                        PF00047; ig; 3.
7; SM00060; FN3; 1.
8; SM00408; IGC2; 3
                                       PS50835; IG_LIKE; 3.
Å,
                   domain
  60087 MW;
D5E81D9E5574E9DE CRC64;
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RESULT 47
Q96RW7
ID Q96RV
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Best Local S
Matches 50
Query Match
                                                                                                                                                                                                                                                                 Pfam; PF00008; EGF; 5.
Pfam; PF000047; ig; 44.
Pfam; PF00090; tep 1; 6.
SMART; SM00179; EGF CA; 7.
SMART; SM00209; TSP1; 6.
SMART; SM00209; TSP1; 6.
SMART; SM00329; VWA; 1.
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Q96RW7;
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0005727; GO; GO:0005509; FGO; GO:0004197; FGO; GO:0006508; FGO:0006508; FGO:0006
                                                                PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
EGF-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
InterPro;
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01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Human hemicentin gene.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hemicentin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                              SEQUENCE
                                                                                                                                                                                                    PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR0001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  L; AF156100; AAK68690.1; GO:0005727; C:extrachromosomal circu GO:0005509; F:calcium ion binding; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             135 RRGTNVLTASN--IMVTR------DERVRLID--GYNLEISDLEPQDAGDYVCQISD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50;
                                                                                 969; TIGR01451; B ant repeat; 9
3; PS00010; ASX_HYDROXYL; 5.
3; PS00268; CECRODIN; 1.
3; PS01186; EGF_2; 3.
3; PS01187; EGF_CA; 8.
3; PS01187; EGF_CA; 8.
44.
45; PS00639; THIOL PROTEASE_HIS
3; PS00639; THIOL PROTEASE_HIS
3; PS00639; TRIOL PROTEASE_HIS
45; PS50092; TSP1; 6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | IPR001434; DUF11.
| IPR001881; EGF Ca.
| IPR006209; EGF_like.
| IPR009017; GFF_like.
| IPR007110; Ig-Tike.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TARIGDGPILTLEKLERQQAGVYQCTADNGVGDPVTVDMRLDVL
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IPR000875; Cecropin.
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                                            Immunoglobulin domain
A; 613660 MW; F000B
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Pred. No. 0.022
36; Mismatches
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                                            F000B319CED7B52C CRC64;
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21173196; PubMed=11275258;
Kumarcean P.R., Stepp S.E., Verrett P.C., Chuang S.S., Boles K.
Lai W.C., Ryan J.C., Bennett M., Kumar V., Mathew P.A.;
"Molecular characterization of the rat NK cell receptor 2B4.";
mol. Immunol. 37:735-744(2000).
EMBL; AF209406; AAG35766.1; -.
GO; GO:0004872; F:receptor activity; IEA.
InterPro; IPR003599; Ig.
InterPro; IPR003199; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
Eukaryota; Metazos; Chordata;
Mammalla; Eutheria; Rodentia;
NCBI TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9EQK9;
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1-MAR-2001 (TrEMBLrel. 16,
1-OCT-2003 (TrEMBLrel. 25,
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21.1%;
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Sciurognathi; Muridae;
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                                                                                                                                      Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
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Q98921;
Q1-FEB-1997 (TrEMBLrel. 02,
01-FEB-1997 (TrEMBLrel. 02,
01-OCT-2003 (TrEMBLrel. 25,
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SEQUENCE
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SMART; SM00408; IGc2; 1.
PROSITE; PS50835; IG LIKE; 5.
Immunoglobulin domain; Signal
SIGNAL
35
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STRAIN=H.B19ov+; TISSUE=Thymus;
MEDLINE=97133433; PubMed=8978830;
SEQUENCE FROM N.A.
STRAIN=H.B19ov+; TISSUE=Thymus;
MEDLINE=97133433; PubMed=8978830;
                                                                                                                                                                                                                 HEMCAM precursor
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J. Cell Biol. 135:1655-1668(1996)
EMBL; Y08854; CAA70079.1;
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Gallus gallus (Chicken).
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01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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InterPro; IPR003598; Ig_c2.
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Aves; Neognathae; Galliformes; Phasianidae; Phasiani
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InterPro; IPR003598; Ig_c2.
Pfam; PF00047; Ig; 4.
SMART; SM00408; IGc2; 1.
PR0SITE; PS50835; IG LIKE; 4.
Immunoglobulin domain.
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01-NOV-1996
01-OCT-2003
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MEDLINE=96081930; PubMed=7499388;
Taira E., Nagino T., Taniura H.,
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EMBL; Y08856; CAA70081.1; -.
                                                                                                                                     EMBL; D38559; BAA07563.1; -. PIR; I50419; I50419.
                                                                                                                                                                                "Expression and functional analysis of a immunoglobulin superfamily cell adhesion J. Biol. Chem. 270:28681-28687(1995).
                                                                                                                                                                                                                                                         Higuchi H.,
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STRAIN=Leghorn; TISSUE=Gizzard;
MEDLINE=94213753; PubMed=8161457;
Taira E , Takaha N., Taniura H.,
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasiani
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InterPro; IPR003598; Ig_c2.
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MART; SM00408; IGc2; 1.
PROSITE; PS50835; IG_LIKE; 5.
Immunoglobulin domain; Signal
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                                                                                                                                                                                                                                                         Miki N.;
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; 5972D946604AF6F3 CRC64;
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SMART; SM00408; IGc2; 1.
PROSITE; PS50835; IG_LIKE; 5.
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MEDLINE=97133433; PubMed=8978830;
Vainio O., Dunon D., Aissi F., Da
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01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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EMBL; Y08855; CAA70080.1; -.
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InterPro; IPR003598; Ig_c2.
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                                                                                           EPSSPLH---EGDSVRLSCTAHSPVKLDYQWRDARGRKVAEGNQLLLTNLTFETSSNFSCR
                                                                                                                                   TANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCT
                                                                                                                                                                                  SWODMTSLADTNDGVLMLHNVSKSSSGLYRCQTLDLDDMTQHEGDVELVVNYIEGVQVKM
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a; Aves; Neognathae;
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Last annotation updat
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Pred. No. 0.
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; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         27F8F2F47044E163 CRC64;
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expressed by
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c-kit+ progen
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RESULT: 53
Q90880
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Q9NR99
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Best Local
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InterPro; IPR003598; Ig_c2.
Pfam; PF00047; ig; 4.
SMART; SM00408; IGc2; 1.
PROSITE; PS50835; IG LIKE; 4.
Immunoglobulin domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q90880;
01-NOV-1996 (TrEMBLrel.
01-NOV-1996 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
TISSUE-Placenta;
Crowl R.M., Luk D.;
"Identification of the gene encoding Adlican,
expressed in human arthritic tissues.";
submitted (MAR-2000) to the EMBL/GenBank/DDBJ
                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Leghorn; TISSUE=Gizzard;
MEDLINE=96081930; PubMed=7499988;
Taira E. Nagino T. Taniura H...
Higuchi H., Miki N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q90880
                                                                                                                                                                                                                                                                               01-OCT-2000
01-OCT-2003
                                                                                                                                                                                                                                                                                                                         Q9NR99;
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                       Q9NR 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Expression and functional analysis of a immunoglobulin superfamily cell adhesion J. Biol. Chem. 270:28681-28687 (1995).
EMBL; D49849; BAA08648.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     L-gicerin
                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                   Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCT 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VKARSVPGLEQSKQVAVAVKGKPRIVAISAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EPSSPLH--EGDSVRLSCTAHSPVKLDYQWRDARGRKVAEGNQLLLTNLTFETSSNFSCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SWQDMTSLADTNDGVLMLHNVSKSSSGLYRCQTLDLDDMTQHEGDVELVVNYIEGVQVKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVED-----QKEEVQLLV-----FGL 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLND
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illarity 23.7%;
Conservative 3
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(TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                       Chordata;
Primates;
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Pred. No. 0.03;
30; Mismatches
                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                         Created)
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Last annotation updat
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                                                                                                                                                                                       Craniata; Vertebrata;
Catarrhini; Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C4791EEC2EC55133 CRC64;
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Query Match
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SMART; SM00408; IGC2; 10.
SMART; SM00082; LRRCT; 1.
SMART; SM00013; LRRNT; 1.
SMART; SM00013; LRR TYP; 3.
PROSITE; PS50035; IG LIKE; 12.
Immunoglobulin domain.
                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2003 (Tr
SC:dZ263J20.6 (
SC:DZ263J20.6.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8UV52;
Q8UV52;
01-MAR-2002
01-MAR-2002
                                      Receptor.
SEQUENCE
                                                                                                                                                              Hammond S.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ EMBL; AL591476; CAD21600.1; -.
GO; GO:0004872; F:receptor activity; IEA.
                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Actinopterygii; Neopterygii; Cyprinidae; Danio.
                                                                                            InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
Pfam; PF00047; ig; 2.
SWART; SW00409; IG; 2.
                                                                                                                                                                                                                                                                                                                                                                Brachydanio rerio (Zebrafish)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF245505;
HSSP; P56276; 1
                                                                          PROSITE;
                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                    NCBI_TaxID=7955;
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                                                                          PS50835;
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ilarity 23.1%;
Conservative 3
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                                      ΑĄ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAF86402.1;
                                                                          IG_LIKE;
                                        36190 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ig-like.
Ig_c2.
LRR.
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  9.48;
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Pred. No. 0.21;
6; Mismatches
  Score 124;
                                                                                                                                                                                                                                                                                                                              ; Craniata;
Teleostei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                    (Danio rerio).
                                        01F5BCE2055EE064
                                                                                                                                                                                                                                                                                                                                                                                                                          sequence update) annotation update)
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                                                                                                                                                                                                                                                                                                                            Vertebrata; El Ostariophysi;
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Best Local S
Matches 43
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Nucleotide sequence of rat vascular cell adhesion molecule-1 cDNA."; Biochim. Biophys. Acta 1131:214-216(1992).
EMBL; X63722; CAA45254.1; -.
HSSP; P19320; IVCA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Williams A.J., Atkins R.C., Cybulsky M.I., Collins T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Sprague Dawley; TISSUE=Lung; MEDLINE=92305064; PubMed=1377031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vascular cell adhesion molecule 1 precursor.
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Interpro; IPR003598; Ig c2.
Interpro; IPR003989; VCAM-1.
Pfam; PP00047. 4-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO; GO:0016020; C:membrane; GO; GO:0016337; P:cell-cell
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InterPro; IPR007110; Ig-1ike.
InterPro; IPR003598; Ig_c2.
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                        93
                                                                                                                                                                                                                                                                                                                                             ; PR01472; ICAMVCAM1.
; PR01474; VCAM1.
SM00408; IGC2; 4.
E; PS50835; IG_LIKE; 5.
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PLIKNIKIEDSDTYICE----VEDQKEEVQLLV-----FGLTANSDTHLLQGQSLTLT 142
                                                                     EGAAVTMTCASEGLPAPEIFWSKK--
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                                                                                                              KGDTVELTCTASOKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNF
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                                                                                                                                                            Score 124; DE
Pred. No. 0.04
30; Mismatches
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                                                                                                                                                                                                                                                                             POTENTIAL.
VASCULAR CELL ADHESION MOLECULE
                                                                                                                                                                                                                                                       A5AAD1172F67FB96 CRC64;
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      PARRARA RANGARA RANGAR
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Q9VLF0;
01-MAY-2000
01-JUN-2003
01-OCT-2003
Misra S., Crosby M.A., Matthews B.B., Hradecky P., Huang Y., Kaminker J.S., Tupy J.L., Bergman C.M., Berman B.P., Clamp M.E., Drysdale R.A., Emmert D., Harris N.L., Kronmiller B., Marshall E
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta;
Neoptera; Endopteryota; Diptera; Brachycera; Musco
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                       Science
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Bayraktaroglu L., Campbell K., Prochnik S.E., Smith C.D., Carlson J.W., Celniker S.E., Frise E., de Grey A.D.N.J., B., Millburn G.H., Richter J.,
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                                                                                             TISSUE-Human amygdala;
TISSUE-Human amygdala;
Ansorge W., Krieger S., Regiert T., Rittmueller C., Schwager B.,
Ansorge H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann
Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BX538014; CAD97961.1; -.
                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                    01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein DKFZp686B1946 (Fragment).
                                                              SEQUENCE
                                                                          Hypothetical protein.
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                                                            67CA457F160FAD15 CRC64;
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 93; Indels
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| 492 KITLAPSNADVTVGENATMQCNASHDPTLDLSYIWSLNGFPIEFDMEDRHYERAI 546 | 3NNSRVSIWDDGSLEILNITKLDEGSYTCYAENDRGKANGTAVLSVIAAT 49 | 1 KGPSKLNDRADSRRSLWDQGNFPLIIKVLKIEDSDTYICEVEDQKEEVQ-LLVFGLTANS 12 | 11 LLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLT 70 | Match 9.3%; Score 122; DB 13; Length 1009;<br>Local Similarity 21.5%; Pred. No. 0.092;<br>es 51; Conservative 28; Mismatches 94; Indels 64; Gaps 7; | am; PP00047; ig; 6. am; PP00047; ig; 6. ART; SM00060; FN3; 4. ART; SM00408; IGC2; 3. OSITE; PS50835; IG LIKE; 6. munoglobulin domain. QUENCE 1009 AA; 112659 MW; 4264D038E0D225F8 CRC64;   | IPR003961; FN I<br>IPR008957; FN I<br>IPR007110; IG-1<br>IPR003598; IG_C   | ; TISSUE=Brain; ; TISSUE=Brain; 3., Fujita N., Tak coning and express ession molecule, co ii. 13:813-820(19) ii. 13:813-820(20)  | QUENCE FROM N.A. RAIN=J; TISSUE=Brain; gata S., Suzuki A.; bmitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.   | nopus laevis (African clawed frog).<br>nopus laevis (African clawed frog).<br>karyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;<br>phibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;<br>nopodinae; Xenopus.<br>BI_TaxID=8355;  | 9 9 0 1   | 59<br>3250 PRELIMINARY; PRT; 1009 AA.  | :05 SAENDVSFPDVKKVKVVVNFAPTIQEIKSGTVTPGRSGLIRCEGAGVPPP 25  | 45 ISNUMIVNEGINVILITCHATGKPEPSISWRHISPSAKPFENGQYLUIYGITRUQAGEYEC 20  | 28 -NSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTC 18           | 7 LNKRDYSLQIQNVDVTDDGPYTCSVQTQHTPRTWQVH-LTVQVPPKIYD 1  | 6 LNDRADSRRSLWDOGNFPLIIKNLKIEDSDTYICEVEDOKEEVOLLVFGLTA 1  | 20 PAATQGSKVVJJAKGJIVELICTASQKSSIQFHWKANGIKLIGNQGSFLIKGFSK /5 |
|   |   | 443NNSRVSIWDDGSLBIHNIINHDEGSIICIAENDRGAANGIAVLSVIAAI 49           | 71 KGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQ-LLVFGLTANS 12 | 11 LLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKIIGNQGSFLT 70  | Query Match  9.3%; Score 122; DB 13; Length 1009;  Best Local Similarity 21.5%; Pred. No. 0.092;  Best Local Similarity 21.5%; Pred. No. 0.092;  Matches 51; Conservative 28; Mismatches 94; Indels 64; Gaps 7  11 LLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLT 70 | PEAM; P00047; ig; 6.  SMART; SM00408; FN3; 4.  SMART; SM00408; IGC2; 3.  SMART; SM00408; IGC2; 3.  SMART; SM00408; IGC2; 3.  PROSITE; PS50835; IG_LIKE; 6.  Immunoglobulin domain.  SEQUENCE 1009 AA; 112659 MW; 4264D038E0D225F8 CRC64;  Duery Match  Best Local Similarity 21.5%; Pred. No. 0.092;  Best Local Similarity 21.5%; Mismatches 94; Indels 64; Gaps 7  Matches 51; Conservative 28; Mismatches 94; Indels 64; Gaps 7  11 LLVLQLALLPAATQGNKVVLGKKGDTVELTCTASOKKSIOFHWKNSNQIKILGNQGSFLT 70 | InterPro; IPR003961; FN_III. InterPro; IPR003961; FN_IIIlike. InterPro; IPR003961; FN_IIIlike. InterPro; IPR003957; FN_IIIlike. InterPro; IPR003598; Ig_c2. Pfam; PP00041; fn3; 4. Pfam; PP00041; fn3; 4. Pfam; PP00041; fn3; 4. SMART; SM00060; FN3; 4. SMART; SM00060; FN3; 4. SMART; SM00060; FN3; 4. SEQUENCE 1009 AA; 112659 MW; 4264D038E0D225F8 CRC64; SMART; SM00408; IG_c; 1009 AA; 112659 MW; 4264D038E0D225F8 CRC64; SMART; SM00408; IG_c; 1009 AA; 112659 MW; 4264D038E0D225F8 CRC64; SMART; SM00408; IG_c; 1009 AA; 112659 MW; 4264D038E0D225F8 CRC64; SMART; SM00408; IG_c; 1009 AA; 112659 MW; 4264D038E0D225F8 CRC64; SMART; SM00408; IG_c; 1009 AA; 112659 MW; 4264D038E0D225F8 CRC64; SMART; SM00408; IG_c; 1009 AA; 112659 MW; 4264D038E0D225F8 CRC64; SMART; SM00408; IG_c; 1009 AA; 112659 MW; 4264D038E0D225F8 CRC64; SMART; SM00408; IG_c; 1009 AA; 112659 MW; 4264D038E0D225F8 CRC64; SMART; SM00408; IG_c; 1009 AA; 112659 MW; 4264D038E0D225F8 CRC64; SMART; SM00408; IG_c; 1009 AA; 112659 MW; 4264D038E0D225F8 CRC64; SMART; SM00408; IG_c; 1009 AA; 112659 MW; 4264D038E0D225F8 CRC64; SMART; SM00408; IG_c; 1009 AA; 112659 MW; 4264D038E0D225F8 CRC64; SMART; SM00408; IG_c; 1009 AA; 112659 MW; 4264D038E0D225F8 CRC64; SMART; SM00408; IG_c; 1009 AA; 112659 MW; 4264D038E0D225F8 CRC64; SMART; SM00408; IG_c; 1009 AA; 112659 MW; 4264D038E0D225F8 CRC64; SMART; SM00408; IG_c; 1009 AA; 112659 MW; 4264D038E0D225F8 CRC64 | SEQUENCE FROM N.A.  STRAIN=1; TISSUEB-Brain; Nagata S., Fujita N., Takeuchi K., Watanabe K.; "CDNA cloning and expression of the Xenopus homologue of the neural cell adhesion molecule, contactin (F3/F11)."; Zool. Sci. 13:813-820(1997). EMBL; AB015205; BAAL8780.1; InterPro; IPR003951; FN_III-like. InterPro; IPR003951; FN_III-like. InterPro; IPR003959; FN_III-like. InterPro; IPR003598; IG_C2. Pfam; PF00041; ig; 6. SMART; SM00408; IGc2; 3. Pfam; PF00047; ig; 6. SMART; SM00408; IGc2; 3. SMART; SM00408; IGc2; 3. SMART; SM00408; IGc2; 3. SMO0408; IGc2; 3. SMART; SM00408; IGc2; IGc2 SMART; SM00408; IGc2 SMART; SM00408; IGc2 SMART; SM00408; IGc2 SMART; SM00408; IGc2 SMART | SEQUENCE FROM N.A.  STRAIN=; TISSUE-Brain; Nagata S., Suzuki A.; S | Eukaryota; (African clawed frog).  Eukaryota; Metazoa; Chordata; Cranilata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;  Xenopodinae; Xenopus.  [1] TaxID=8355; [1] TaxID=8355; [1] TisSUE=Brain;  Nagata S., Suzuki A.;  SEQUENCE FROM N.A.  STRAIN-J; TISSUE-Brain;  Nagata S., Pujita N., Takeuchi K., Watanabe K.;  SEQUENCE FROM N.A.  SEQUENCE IN THE SEQUENCE FROM N.A.  SEQUENCE FROM | Ol-NOV-1998 (TIEMBLrel. 08, Created) Ol-NOV-1998 (TIEMBLrel. 28, Last sequence update) Ol-NOV-1998 (TIEMBLrel. 25, Last annotation update) Ol-OCT-2003 (TIEMBLrel. 25, Last annotation update) OL-OCT-2003 (TIEMBLrel. 25, Last annotation update) Contactin A. Xenopus laevis (African clawed frog). Enkaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopus laevis (African clawed frog). Enkaryota, Metazoa; Chordata; Craniata; Pipoidea; Pipidae; Xenopus laevis (African clawed frog). Enkaryota, Metazoa; Chordata; Craniata; Pipoidea; Pipidae; Xenopus laevis (African clawed frog). Enkaryota, Metazoa; Chordata; Craniata; Pipoidea; Pipidae; Xenopus laevis (African clawed frog). Enkaryota, Metazoa; Chordata; Craniata; Pipoidea; Pipidae; Xenopus laevis (African clawed frog). InterPro; ITISUEE-Brain; Nagata S., Suzuki A. STRAIN-3; TISSUE-Brain; Nagata S., Suzuki A. STRAIN-3; TISSUE-Brain; Nagata S., Fujita N. Taksuchi K., Watanabe K.; SEQUENCE FROM N.A. STRAIN-3; TISSUE-Brain; Nagata S., Fujita N. Taksuchi K., Watanabe K.; Nagata S., Fujita N., Taksuchi K., Watanabe K.; SEQUENCE FROM N.A. STRAIN-3; TISSUE-Brain; Nagata S., Fujita N., Taksuchi K., Watanabe K.; Nagata S., Fujita N., Taksuchi K., Wata | SULT 59  2050  PRELIMINARY; PRT; 1009 AA.  03250; 01-NOV-1998 (TrEMBLrel. 08, Last sequence update) 01-NOV-1998 (TrEMBLrel. 08, Last sequence update) 01-NOV-1998 (TrEMBLrel. 25, Last sequence upda | SULT 59 205 SAENDVSFPDVRKVKVVNPAPTICEIKSGTVTPGRSGLIRCEGAGVPPP 254 205 SAENDVSFPDVRKVKVVNPAPTICEIKSGTVTPGRSGLIRCEGAGVPPP 254 2050 2050 2050 2050 2050 2050 2050 2 | 143 ISNUMYNNGTNYTLICLATIGREEPS LEWRHILSPSAKEPENGTUDIG TRUQUAREE 208 185 TV | 128 -NSDTHLLGGSLTLTESPPGSSPSVOCR - SPECKNIGGKTLSVSCIELODGGTWTC 184 145 ISNDWTVNBGTWTLTCLATGKDEDSTSWHHISPSAKEPENGGKTLSVSCIELODGGTWTC 184 185 TV | 128 - NSDPHLLQQQSLTITUESSPESSPSVQCESPRGKNIQGGTTSVSQLELDDSGTWC 124  128 - NSDPHLLQQQSLTITUESSPGSSPSVQCESPRGKNIQGGTTSVSQLELDDSGTWC 124  128 - STRUMTNEGTNVTLTCLATGKEEPSISWHISPSAKEFENQQYLDIVGTTRDAGEYEC 204  185 TV | 97 LNRA   |

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547

RLPLQNDV--GSELIIKNAQLKHAGRYTCTAQTIVDNSSASADLVVRGP--PGPPGG

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RESULT
Q8HYV1
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Best Local (
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SMART; SM00409; IG; 5.
SMART; SM00409; IG; 5.
SMART; SM00137; MAM; 1.
PROSITE; PS500835; IG LIKE; 5.
PROSITE; PS50080; MAM 2; 1.
NON TER
SEQUENCE 885 AA; 97766 MW;
Eukaryota; Metāzoa; C
Mammalia; Eutheria; C
NCBI_TaxID=9823;
[1]
                                                                                                                 Q8HYV2;
Q8HYV2;
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kierstein S., Al-Bayati H., Kollers S., Brenig B "Assignment of the porcine MAM domain containing glycosylphosphatidylinositol anchor 1 (mdgal) on in stiu hybridisation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2003 (TYEMBLrel. 23, Created)
01-MAR-2003 (TYEMBLrel. 23, Last sequence update)
01-CCT-2003 (TYEMBLrel. 25, Last annotation update)
Glycosylphosphatidylinositol anchor 1 protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted OCT-2002) to the EMBL/GenBank/DDBJ databases EMBL; AJ459296; CAD30702.2; -. GO; GO:0016020; C:membrane; IEA. InterPro; IPR008957; FN_III-like.
                                                                 MDGA1
                                                                                          MAM domain containing
                                                                                                       01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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InterPro; IPR007110; Ig-1ike.
InterPro; IPR003598; Ig_c2.
InterPro; IPR000998; MAM_domain.
Pfam; PF00047; ig; 5.
Pfam; PF00629; MAM; 1.
                                                                            (Fragment).
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                                                   scrofa (Pig)
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                                                                                                                                                                                                                          186
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                                                                                                                                                                                                                          ENVTVQCLLQGGDPLTQLQWSHGPGPLPLGALAQGG-TLSIPSVQARDSGYYNCTATINN
                                                                                                                                                                                                                                                    SSPSVQC----
                                                                                                                                                                                                                                                                             KLKDLRPQEYASLTCQVSDGSVCGIPDKAVTLRLTSTTAPPALKL----SVNETLVVNPG
                                                                                                                                                                                                                                                                                                                              TVFLRCTVNSNPPARFIWKRGSD------
                                                                                                                                                                                                                                                                                                                                                        TVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLI
                                                                                                                                                                                                                                                                                                                                                                                                                                     885 AA; 97766 MW; BC2929D59C3491C5 CRC64;
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                                                                                       (TIEMBLIEL 23, Created)
(TIEMBLIEL 23, Last sequence update)
(TIEMBLE 25, Last annotation update)
(TIEMBLIEL 25, Last annotation update)
containing glycosylphosphatidylinositol
                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                              9.2%;
                         Chordata; Craniata; Vertebrata; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                  24;
                                                                                                                                                                                                                                                                                                                                                                                              Score 121; DB 6
Pred. No. 0.094;
                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                   -RSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQN 189
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                                                                                           anchor
                                         Euteleostomi;
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RESULT 62
P79921
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                                                                                                                                                                                                                                          P SEQUENCE FROM N.A.

C STRAIN=J Strain; TISSUE=Brain;
A Magata S., Fujita N., Takeuchi K., Watanabe K.;
A Nagata S., Fujita N., Takeuchi K., Watanabe K.;
A Coll actioning and expression of the Xenopus homologue of cell adhesion molecule, contactin (F3/F11).";
L Zool. Sci. 13:813-820(1997).
R EMBL; D86505; BAA13100.1; -.
R InterPro; IPR003961; FN III.
R InterPro; IPR003957; FN III-like.
R InterPro; IPR003598; IS_III-like.
R InterPro; IPR003598; Ig_c2.
R InterPro; IPR003598; Ig_c2.
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Best Local S
Matches 47
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"Assignment of the porcine MAM domain containing
glycosylphosphatidylinositol anchor 1 (MDGA1) on chromosome
by in situ hybridisation.";
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ459295; CAD30701.2; -.

GO; GO:0016020; C:membrane; IEA.
InterPro; IPR008557; FN_III-like.
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003598; MAM_domain.

InterPro; IPR003598; MAM_domain.
                                                               Pfam; PF00041; fn3; 4.

Pfam; PF00047; i9; 6.

SMART; SM00060; FN3; 4.

SMART; SM00408; IGC2; 5.

PROSITE; PS50835; IG_LIKE; 6
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SMART; SM00409; IG; 5.
SMART; SM00408; IGc2; 5.
SMART; SM00137; MAM; 1.
PROSITE; PS50835; IG LIKE; 5
PROSITE; PS50860; MAM 2; 1.
NON TER
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P79921;
01-MAY-1997
PROSITE; PS5(Immunoglobul: SEQUENCE 1
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Amphibia; Batrachia; Anura;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=8355;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 131 KLKDLRPQEYASLTCQVSDGSVCGIPDKAVTLRLTSTTAPPALKL----SVNETLVVNPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96
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       1005
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26.3%; Pred. No. 0.09
cive 24; Mismatches
       111665 MW;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
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       6F1CE811F8D97DFE CRC64;
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ia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ₿
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                                              Query Match
Best Local S
Matches 60
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                                                                                                                   Pfam; PF00560; LRR; 14.
Pfam; PF01463; LRRCT; 1.
Pfam; PF01462; LRRNT; 1.
PRINTS; PR00019; LEURICHRPT.
SMART; SM00408; IGC2; 3.
SMART; SM000013; LRRCT; 1.
SMART; SM00013; LRRUT; 1.
SMART; SM00013; LRRUT; 4.
PROSITE; PS00835; IG_LIKE; 3.
                                                                                                                                                                                                                                       InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig_c2.
InterPro; IPR001611; LRR.
InterPro; IPR000483; LRR. Cterm.
InterPro; IPR000372; LRR_Nterm.
InterPro; IPR000372; LRR_typ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P70193;
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"CDNA cloning of a novel membrane glycoprotein that is expressed
specifically in glial cells in the mouse brain LIG-1: A protein v
leucine-rich repeats and immunoglobulin-like domains.";
J. Biol. Chem. 271:22522-22527 (1996).
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01-OCT-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FKUM N.A.
MEDLINE=96394313; PubMed=8798419;
TOhvama M., Wanaka
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                           PIR; A58532
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LRIG1 OR IMG.
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                                               60; Conserv
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 LTVNVLPSFTKIPHDIAIRTGTTARLECAATGHPNPQIAWQKDGG--
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                                             Score 120; DB 1
Pred. No. 0.15;
40; Mismatches 1
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Pred. No. 0.
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                                         RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D. Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfelffer B.D.,
RA Barandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfelffer B.D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Durbin K., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Harris N., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA McIntosh T., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Mount K.A., Nowins K., Nusskern D.R., Paeleb J.M.,
RA Shie B.C., Siden-Kiamos I., Simpson M., Strong R., Smith T.,
Ra Spier E., Spradling A.C., Stapleton M., Strong R., Smith T.,
Ra Harls R., Schales R., Fettor C., Turner R., Venter E., Wang A.H., Wang X.,
                           Spier E., (
Svirskas R
Wang Z.Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              097394
097394;
01-MAY-1999
01-MAY-1999
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01-MAY-1999 (TrEMBLrel. 25, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
SIDEKICK protein (CG5227-PA) (CG5227
SDK OR BCDNA:LD22322 OR CG5227.
Drosophila melanogaster (Fruit fly).
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s R., IC.
Y., Wassarman
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                           Venter E., Wang A.H
ck G.M., Weissenbach
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                                                                                                                                                                                               b J.M.,
Reese M.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                      Ketchum K.A.,
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Pfam; PF00047; ig; 5.

PRINTS; PR00014; FNTYPPIII.

SMART; SM00060; FN3; 13.

SMART; SM0040B; IGC2; 4.

SMART; SM0040B; IGC2; 4.

PROSITE; PS50835; IG_LIKE; 5.

Immunoglobulin domain; Repeat.
SEQUENCE 2222 AA; 246174 MW;
Q9JLM2
Q9JLM2;
01-OCT-2000
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EMBL; AE003418; AAF45541.3;
PIR; T13924; T11924
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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InterPro; IPR003961; FN III.
InterPro; IPR003957; FN III-like.
InterPro; IPR007110; Ig-like.
InterPro; IPR005598; Ig_c2.
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FlyBase; FBgn0021764; sdk.
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EMBL; AF156989; AAF71162.1; -.. GO; GO:0004872; F:receptor activity; IE
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Q9W6V2;
01-NOV-1999
01-NOV-1999
01-OCT-2003
MEDLINE=99264333; PubMed=10330412;
Marg A., Sirim P., Spaltmann F., Plagge
Mathjen F.G., Brummendorf T.;
"Neurotractin, A novel neurite outgrowth
that interacts with CEPU-1 and LAMP.";
J. Cell Biol. 145:865-876(1999).
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                Gallus gallus (Chicken).
Bukaryota; Metazoa; Chordata;
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SMART; SMOO409;
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00409; IG; 1
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Sciurognathi; Muridae; Murinae; Rattus.
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; Galliformes; Phasianidae; Phasianinae;
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                      outgrowth-promoting LAMP.";
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Best Local S
Matches 51
Query Match
Best Local Similarity
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InterPro; IPR003598; Ig_c2.
Pfam; PPR0047; ig; 3.
SMART; SM00408; IGc2; 2.
PROSITE; PS50835; IG LIKE; 3.
Immunoglobulin domain.
SEQUENCE 352 AA; 37944 MW;
                                                                                                                              Pfam; PF00041; fn3; 3.
Pfam; PF00041; fg; 5;
Pfam; PF00041; fg; FNTYPEII
PRINTS; PR00014; FNTYPEII
SMART; SM00000; FN3; 3.
SMART; SM00408; IGC2; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=98117249; PubMed=9458045; Kidd T., Brose K., Mitchell K.J., Goodman C.S., Tear G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Hexapoda, Inse
Neoptera, Endopterygota, Diptera, Brachycera,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Roundabout controls axon crossing of the CNS midline and defines novel subfamily of evolutionarily conserved guidance receptors."; Cell 92:205-215(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-1998 (TrEMBLrel.
01-JUN-1998 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
ROUNDABOUT 1.
                                                                   Immunoglobul
SEQUENCE 1
                                                                                                                                                                                                                                          InterPro; IPR003961; FN III-
InterPro; IPR008957; FN III-like.
InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig-c2.
                                                                                                                                                                                                                                                                                                                                                                                                         FlyBase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              044924
                                                                                                                                                                                                                                                                                                                                   FlyBase; FBgn0005631; robo.
30; GO:0005886; C:plasma membrane;
30; GO:0007411; P.axon guidance; It
InterPro; IFR003962; FnIII_subd.
                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P56276; 1TLK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF040989; AAC38849.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ROBO OR ROBO1 OR CG13521.
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                                                                                    PS50835; IG_LIKE; 5.
bulin domain; Repeat
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larity 22.1%;
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Pred. No.
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No. 0.
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                  Length 1395;
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RESULT 69
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Q8AW79;
01-MAR-2003
01-MAR-2003
                                                                                                                                                                                                                                                                                                       Receptor.
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
Pfam; PF00047; Ig; 2.
SMART; SM00409; IG; 2.
                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (DEC-2002) to the EMBL/GenBank/DDBJ EMBL; AL591405; CAD58990.1; -. GO:0004872; F:receptor activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Garner P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cyprinidae; Dani
NCBI_TaxID=7955;
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01_MAR-2003 (TrEMBLrel. 23, Last se
01_CCT-2003 (TrEMBLrel. 25, Last an
01_CCT-2003 (TrEMBLrel. 25, Last an
SI:dZ125J23.8.1 (Novel immune-type
                                                                                                                                                                                                                                                                                                                                           PROSITE;
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53; Conservative
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                                                                                                                                                                                                      QENNVKIVQAGEDVNLTCTESPNMQLSTAWFKHTADGKTLQIVEN--LFFTKSPIWNNNV 78
                                                                                                         AATDRNRTLHOSLIDTVD--PGDSVNLQCSIFTESCAGDHSIYWFKQSSGDSEGVLYTKG
                                                                                                                                                                                SKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGL-----T 126
                                                                                                                                                                                                                                QGNKVVLGKKGDTVELTCTASQKKSIQFHW----KNSNQIKILGNQGSFLTKGP-----
                                                                                                                                                                                                                                                                                                                                           PS50835;
                                                                                                                                 ANSDTHLLQGQSLTLTLESPPGSSPSVQC------
                                                                                                                                                         EKMND----VNVIIEEGYFNLTILKTNPSDSATYYCVV----SSYEAIGMGLGSRLIVRD 130
                                                                                  -RSPRGKNIQGGKT----
                                                          ERNGRCKNSAESETQSCVYSLHKNNISRSDTGIYYCAV
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276 i
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Last annotation update)
ne-type receptor 1.8, va
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Pred. No. 0.03
26; Mismatches
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Q8AW80

PRELIMINARY;

PRT;

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RESULT 70
Q9Y3Y8
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Best Local
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01-NOV-1999 (TrEMBLrel. 12,
01-OCT-2003 (TrEMBLrel. 25,
Hypothetical protein 'P---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8AW80;

01-MAR-2003 (TrEMBLrel. 23, Created)

01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

01-OCT-2003 (TrEMBLrel. 25, Last annotation updat

SI:dZ125J23.8.2 (Novel immune-type receptor 1.8,
                                                                                                                                                                                                                                    Q9Y3Y8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (DEC-2002) to the EMBL/GenB EMBL; AL591405; CAD58989.1; -. GO; GO:0004872; F:receptor activity; InterPro; IPR003599; Ig. InterPro; IPR003599; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brachydanio rerio (Zebrafish)
Eukaryota; Metazoa; Chordata;
Actinopterygii; Neopterygii; T
Cyprinidae;
NCBT Talio.
                                                             Wambutt R., Heubner D., Mew Submitted (MAY-1999) to the EMBL; AL049946; CAB43220.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NITRI.8.
                                                                                               TISSUE=Brain;
                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                             DKFZP564I1922.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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SMART; SM00409; IG; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Fragment).
         InterPro; IPR007110; Ig-like
InterPro; IPR003598; Ig_c2.
Pfam; PF00047; ig; 6.
                                           HSSP;
                                                                                                           SEQUENCE FROM N.A.
                                                                                                                               NCBI_TaxID=9606;
                                          T08678; T08678.
; P56276; 1TLK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PS50835; IG_LIKE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             QGNKVVLGKKGDTVELTCTASQKKSIQFHW----KNSNQIKILGNQGSFLTKGP-----
                                                                                                                                                                                                                                                                                                                                             AATDRNRTLHQSLIDTVD--
                                                                                                                                                                                                                                                                                                                                                                                          EKMND----VNVIIEEGYFNLTILKTNPSDSATYYCVV----SSYEAIGMGLGSRLIVRD
                                                                                                                                                                                                                                                                                                                                                                                                                 SKINDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGL-----T
                                                                                                                                                                                                                                                                                                                                                                                                                                       QENNVKIVQAGEDVNLTCTFSBNMQLSTAWFKHTADGKTLQIVFN--LFFTKSPIWNNNV
                                                                                                                                                                                                                                                                                                     ERNGRCKNSAESETQSCVYSLHKNNISRSDTGIYYCAV
                                                                                                                                                                                                                                                                                                                                                                    ANSDTHLLQGQSLTLTLESPPGSSPSVQC-----
                                                                                                                                                                                                                                                                                                                         -RSPRGKNIQGGKT-----
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278 AA;
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                                                                                                                                                                                                                                               PRELIMINARY;
ig; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          278
                                                                                                                                         Chordata;
Primates;
                                                                                                                                                                                     rel. 12, Last (
rel. 25, Last (
) (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9.0%;
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                                                                         the
                                                                                      Mewes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26;
                                                                          es H.W., Gassenhuber J., Wie
EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL/GenBank/DDBJ
                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 118.5; DB Pred. No. 0.034;
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; Craniata; Vertebrata; Euteleostomi;
Teleostei; Ostariophysi; Cypriniformes;
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| PGDSVNLQCSIFTESCAGDHSIYWFKQSSGDSEGVLYTKG
                                                                                                                                                                                                                                                                                                                         LSVSQLELQDSGTWTCTV
                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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on update)
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RESULT

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ID Z24
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문
                                                                            Query Match
Best Local S
Matches 53
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-BALB c; TISSUE-Brain;
Warg A., Sirim P., Spaltmann F.,
Rathjen F.G., Bruemmendorf T.;
"Neurotractin, a novel neurite of
that interacts with CEPU-1 and L.
J. Cell Biol. 4:865-876(1999)
                                                                                                                                                                                                                                  Submitted (MAY-2002) to the EMEL; AJ487032; CAD31699.1; -. InterPro; IPR003599; Ig. InterPro; IPR007110; Ig-like. InterPro; IPR003598; Ig_c2. Pfam; PF00047; Ig; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q80Z24;
Q80Z24;
01-JUN-2003
01-JUN-2003
01-OCT-2003
                                                                                                                                                 Pfam: Fruve.
SMART; SM00409; IG; 3.
SMART; SM00408; IGC2; 3.
PROSITE; PS50835; IG_LIKE; 3.
PROSITE; PA50835; IG_SIKE; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein; NON_TER 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                               Schaefer M.;
                                                                                                                                                                                                                                                                                                                                                                               STRAIN-BALB c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NTRA.
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                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neurotractin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32 KKGDTVELTC----TASQKKSIQFHWKNSNQIKILGNQGSFLT-----KGPSKLND-R
35
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                                                                            l Similarity
53; Conserv
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                                   PAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGP----SK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RLILQLTVLEPMEKPIFHDPISEKITAMAGHTISLNCSAAGTPTPSLVWVLPNGTDLOSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AD---SRRSLWD---
PWAAVDNMLV--RKGDTAVLRCYLEDGAS-KGAWLNRSSIIFAG--GDKWSVDPRVSIST
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                                                                            9.0%;
llarity 23.0%;
Conservative 3
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                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----VSQLELQDSGTWTCTVLQN-----QKKVEFKIDIVPRAS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALPAPPTGSA------LPDPQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63918 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chordata;
Rodentia;
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25,
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                                                                            34;
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Last ann
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Pred. No. 0.09:
38; Mismatches
                                                                                                                                                                                                                                                                                                                       ŀ
                                                                            Score 118; DB
Pred. No. 0.05
34; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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LAMP.";
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No. 0.0
                                                                                               118; DB 1
No. 0.051;
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                                                                                                                  11,
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; Murinae; Mus
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                                                                                                                      348;
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E
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RA Addams M.D., Calniker S.E., Hilt R.A., Sabburner M.A., Galle R.F.,
RA Addams M.D., Calniker S.E., Hilt R.A., Sabburner M.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Burton R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Ballew R.M., Bayers L.A., An H.-J., Andrews-Ffannkoch C., Baldwin D.A.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Boltshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Broketein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Broketein P., Brottier R.,
RA Bortova D., Botchan M.R., Bouck J., Broketein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Kinmel B.E., Kodira C.D., Kratt C., Kravitz S., Kulp D., Lai Z.,
Labako P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Labako P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Menkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Menson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb JM.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Syler B., Syradling A.C., Staplecon M., Skupski M.P., Smith T.,
RA Syler E., Spradling A.C., Staplecon M., Skupski M.P., Smith T.,
RA Shen B.M., Moodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Shen S.H., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Shen S.H., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Shen S.H., Woo
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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01-OCT-2003 (TrEMBLrel.
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Science 287:2185-2195(2000)
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   Adams
   M.D.,
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   Kronmiller
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   K.H.,
   Holt R.A.,
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A Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
A Carlson J.W., Center A., Champe M., Davemport L.B., Dietz S.M.,
A Corlson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
A Perriera S., Frise E., Galle R.F., Garg N.S., George R.A.,
A Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
A Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
A McIncosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,
A McIncosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,
A McIncosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,
A McIncosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,
A McIncosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,
A McIncosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Scheeler F.,
A Phouanenavong S., Pittman G.S., Patel S., Pfeiffer B., Scheeler F.,
A Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
T'Sequencing of Drosophila melanogaster genome.",
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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InterPro; IPR001064; Crystallin.
InterPro; IPR008957; FN_III-like.
InterPro; IPR008957; FS_III-like.
InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig_C2.
Pfam; PF00047; Ig; 3.
SMART; SM00408; IGC2; 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE003595; AAF51754.2;
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                                                                                                                                                                                                                                                                                                                     WDQGNFPLIIKNLKIEDSDTYICEVEDQKEE-----VQLLV----FGLTANSDTHLLQGQ 137
                                                                                                                                                                                                                                                                                                                                                                                             KVIV---GETIELPCKVQNLGSFVLLWRKGS-----SVLTAGHLKIT--RDQRFKI
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D., Celniker S.E.,
                                                                                                                                                                                           SLTLTLESPPGSSPSV-----QCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQK 191
                                                                KVEFKIDI
                                                                                                                                 TVTLECKASGNPVPTIFWFKKDVFSGP--THLSDSSTLILENVDRHHAGTYQCSA-DNGV
                                                                                                                                                                                                                                                     --VGDYNLQINGVKTQDAGDYICQLGDQENRDQVHTVEILVPPTLRALPHNGQVTARKGS
   KDRVSMDI
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e EMBL/GenBank/DDBJ databases
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Pred. No. 0.062;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     campbell K., mith C.D., er S.E.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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RESULT 73 Q9D2Z1 ID Q9D2Z AC Q9D2Z

Q9D2Z1 Q9D2Z1;

PRELIMINARY;

PRT;

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RESULT 74
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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Couackenbush J.,
RA Fleischmann W., Gasaterland T., Gissi C., King B., Kochiwa H.,
RA Fleischmann W., Staubhi F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubhi F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubhi F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Bownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Guetincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Guetincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Guetincich S., Hill D., Hofmann M., Badzierelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y., Storch K., Schoenbach C., Seya T., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y., Storch K., Seya T., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; ig; 4.
SMART; SM00408; IGC2; 2.
PROSITE; PS50835; IG_IKE; 4.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2001
01-JUN-2001
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 409:685-690(2001).
-!- SIMILARITY: CONTAINS 4 IMMUNOGLOBULIN-LIKE EMBL, AK018613; BAB31307.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=C57BL/6J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9130012D09Rik protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hayashizaki Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WGD; MGI:1918851; 9130012D09Rik.
                                                                                                                                                               387
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                                                                                 423
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                                                                                 SSSMSPGATAGIVIGILVATALATGLG
                                                                                                                         AASALPAALA-----VISFLIGLGLG
                                                                                                                                                                                                  SQLELQDSGTWTCTVLQNQKKVEFKIDIVPRASALPAPPTGSALPDPQTASAL---PDPP
                                                                                                                                                                                                                                                                                                                                                                 LTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTAN
                                                                                                                                                                                                                                                                                                                                                                                                                                      VLQLALLPAATQGN----KVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSF
                                                                                                                                                               EALRQEHQGIYSCTSSND-
                                                                                                                                                                                                                                            YGPDQVEITQGPASGVVSTIEAMLNSSLTLYCRADSIPGARYQWTHEHSSKVLDGEQLSI
                                                                                                                                                                                                                                                                                  ---SDTHLLQG--QSLTLTLESPPGSSPSVQCRS-----PRGKNIQGGKTLSV 171
                                                                                                                                                                                                                                                                                                                           LKGQPLRPSDRL----TLSSQ-NRTLTIHGLQRDDIGPYECEVWNWGSQARSVPLKLTIN
                                                                                                                                                                                                                                                                                                                                                                                                         VVKVQVLEKVTAPNIEFPTLALVENATSVTLTCKTSHQR-VGVHW----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63444 MW;
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Last annotation updat
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Pred. No. 0.09
12; Mismatches
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Adachi J., Funur.
An S., Yamanaka
                                                                                                                         249
                                                                                 449
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).099;
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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Raha S.S., McDwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Rilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Raha S.J., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Raha S.J., Marra M.A.;
Nones S.J., Marra M.A.;
Nones S.J., Marra M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00047; ig; 4.
SWART; SW00409; IG; 4.
SMART; SW00408; IG; 4.
PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS00299; IG MHC; 1.
SEQUENCE 577 AA; 53426 MW; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q80Y42
Q80Y42;
Q1-JUN-2003
Q1-JUN-2003
Q1-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-FVB/N; TISSUB-LULLUL, STRAIN-FVB/N; TI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; BC049361; AAH49361.1; -.
InterPro; IPR003599; Ig.
InterPro; IPR00310; Ig-like.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003006; Ig_MHC.
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
TISSUE=Colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Euxaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
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STRAIN=FVB/N; TISSUE=Colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Generation and initial analysis of more than 15,000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13 VLQLALLPAATQGN----KVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
AASALPAALA-----VISFLLGLGLG
                                                                                                             EALRQEHQGIYSCTSSND-
                                                                                                                                                                                                                                                                                                                                                                                                                      LKGQPLRPSDRL----TLSSQ-NRTLTIHGLQRDDIGPYECEVWNWGSQARSVPLKLTIN
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                                                                                                                                                                                       SQLELQDSGTWTCTVLQNQKKVEFKIDIVPRASALPAPPTGSALPDPQTASAL---PDPP
                                                                                                                                                                                                                                                                                                                                           ---SDTHLLQG--QSLTLTLESPPGSSPSVQCRS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTAN
                                                                                                                                                                                                                                                                 YGPDQVEITQGPASGVVSTIEAMLNSSLTLYCRADSIPGARYQWTHEHSSKVLDGEQLSI
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Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 118;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ₽
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                                                                                                                     VTGLA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 577;
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                                                                                                                     -RSASVLVMVVGLQ
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RA Addams M.D., Celnikers S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Addams M.D., Celnikers S.E., Holt R.A., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Burtin G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Ballew R.M., Baster E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Aphayani A., An H. J., Andrews Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Byraktaroglu L., Beasley E.M.,
RA Beceson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Gerry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Burtis K.C., Busam D.A., Butler H., Caddeu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cloden K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Ketchum K.A.,
RA Harris N.L., Marvey D., Heiman T.J., Hernandez J.R., Ketchum K.A.,
RA Harris N.L., Marvey D., Kratif C., Kravizz S., Kullp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Kullp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Kullp D., Lai Z.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshreti A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshreti A.,
RA Merkulov G., Wilshina N.V., Mobarry C., Morris J., Moshreti A.,
RA Merkulov G., Stapleton M., Skupski M.P., Shith T.,
RA Sylers R., Speralling A.C., Stapleton M., Skupski M.P., Shith T.,
RA Mang Z.-Y., Wassarman D.A., Wasnor K., Scheeler F., Shen H.,
RA Maris R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Harris R., P., Pareri J.S., Zhan M., Zhang S., Zhao Q., Zheng L.,
RA La
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Q9W213
      Amanatides P.G., Brandon R.C., Rogers Y., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A., Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M., Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D., Ferriera S., Frise Egalle R.F., Garg N.S., George R.A., Gonzalez M., Houck J., Hoskins R.A., Hostin D., Hwland T.J., Ibeywam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A., McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J., Pacleb J., Paragas Park S., Patel S., Pfeiffer B., Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F., Stapleton M., Strong R., Svirskas R., Tector C., Tyler D., Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
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Q9W213;
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                          SEQUENCE
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1-OCT-2003
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Last
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Q8IRV9;
Q8IRV9;
Q8IRV9;
Q1-MAR-2003
Q1-MAR-2003
Q1-QCT-2003
CG7981-PC.
TROL OR EG:B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; P
PROSITE;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
                                                                                                                                                                                                TROL OR EG:BACR25B3.11 OR CG7981.
Drosophila melanogaster (Fruit fly).
Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Hexapoda, Inse
Neoptera, Endopterygota, Diptera, Brachycera,
Ephydroidea, Drosophilidae, Drosophila.
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mungall C.J., Lewis S.E.;
"Annotation of Drosophila melanogaster genome "Submitted (MAY-2002) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clamp M.E., Drysdale R.A., Emmert D., Frise E., de Grey Harris N.L., Kronmiller B., Marshall B., Milburn G.H., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.J., Yamada C., Ashburner M., Gelbart W.M., Mungall C.J., Lewis S.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO; GO:0005886; C:plasma membrane; IGO; GO:0007411; P:axon guidance; II InterPro; IPR003962; FNIII subd. InterPro; IPR003961; FN III. InterPro; IPR003961; FN III-like. InterPro; IPR008957; FN III-like.
                                                                                           SEQUENCE FROM N.A.
MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00041; fn3; Pfam; PF00047; ig;
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HSSP; P56276; 1TLK
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                                                                                                                                                                             NCBI_TaxID=7227;
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L., Bergman
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C.M., Berman
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25.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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, Prochnik S.E., Smit
, Carlson J.W., Celni
, Frise E., de Grey A
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                                                                                                                                                                                                                            Insecta; Pterygo
era; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                          update)
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., Smith C.D.,
., Celniker S.E.,
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.H., Richter J.,
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RA Abril J.F., Doyle C., Bexter B.G., Melt G., Welson C.R., Gabor G.H., RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D., RA Bellew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., RA Bellew R.M., Botchan M.R., Bouck J., Brokstein P., Brottier P., RA Borkova D., Bucchan M.R., Bouck J., Brokstein P., Brottier A., Chandra I., RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Dodson K., Doup E., Gorrell J.H., Gu Z., Gelbart M.M., Glasser K., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C., RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., Mepareson D., Lai X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Lai S., Walson K.A., Nixon K., Nusskern D.R., Pacleb J.M., RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., RA Rainert K., Remington K.A., Nixon K., Sungskern D.R., Pacleb J.M., RA Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissehard J., RA Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissehach J., RA Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J., "The genome sequence of Drosophila melanogaster."; Snith H.O., Reinstock G.M., Pacle D.C., Snith H.O., Roches G.D., Scheng L., Scheng S., Yao Q.A., Ye J., RA Scheng S., Scheng C., Snith H.O., Reinstock G.M., Weissenbach J., Smith H.O., Scheng L., Schen
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A Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,

A Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,

Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

A Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

A Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,

Friere E., Galle R.F., Garg N.S., George R.A.,

Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,

A Dodson T.C., Moy M., Kruse D., Li P., Mattei B., Moshrefi A.,

McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,

Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,

A Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,

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Abril J.F.
Ballew R.N
                                                                                                                                                                                                                                                                                        Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K., Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.; "Annotation of Drosophila melanogaster genome."; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
FlyBase; FBgn0001402;
GO; GO:0003677; F:DNA
GO; GO:0005198; F:stru
                                                  EMBL; AE003424; AAN09077. FlyBase; FROMOTO
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EMBL/GenBank/DDBJ databases.
activity; IEA
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-Pfannkoch C., Baldwi
ktaroglu L., Beasley
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Baldwin D.,
Beasley E.M.,
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    DAFFEE BROSSOSS
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Best Local S
Matches 45
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Pfam; PF00057; ldl_recept_a; 23
Pfam; PF00057; ldl_recept_a; 23
PRINTS; PR00261; LDaminin_B; 3.
SMART; SM00181; EGF; 9.
SMART; SM00181; EGF; 12.
SMART; SM00409; IG; 12.
SMART; SM00409; IG; 12.
SMART; SM00281; LamB; 3.
SMART; SM00282; LamG; 3.
SMART; SM00282; LamG; 3.
SMART; SM00192; LDLa; 23.
                                                                                                                                   Q9W4Y4;
Q9W4Y4;
01-MAY-2000
01-OCT-2002
01-OCT-2003
              CG7981 protein.
CG7981 protein.
TROL OR EG:BACR25B3.11 OR CG7981.
Drosophila melanogaster (Fruit fly).
Drosophila metazoa; Arthropoda; Hexapoda;
Eukaryota; Metazoa; Arthropoda; Brachyce
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InterPro;
Eukaryota; Metazoa; Arthropoda; Hexapoda; Ins
Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
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Pfam;
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2; PS00022; EGF 1; 10.
3; PS01186; EGF 2; 6.
3; PS01186; IG LIKE; 11.
3; PS01248; LAMININ TYPE EG 2; PS01248; LAM G DOMAIN; 3
2; PS0129; LDLRA 1; 20.
3; PS0129; LDLRA 1; 20.
3; PS00030; RRM RNP 1; 1.
2; PS00030; RRM RNP 1; 1.
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IPR000504;
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laminin_EGF; 2.
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RNA_rec_mot.
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RA Adams M.D., Celniker S.E., Hilt R.A., Evans C.A., Golayne J.D.,
RA Adams M.D., Celniker S.E., Hilt R.A., Ashburner M., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Ballew R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Ffannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Grerry J.M., Cawley S., Dahlke C., Davarstronglu L., Beasley E.M.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gana P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Howland T.J., Wei M.-H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D. Lai Z.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA McIntosh C., Stapleton K., Saunders R.D.C., Scheeler F., Shen H.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Melson D.R., Nelson K.A., Saunders R.D.C., Scheeler F., Shen H.,
RA Melson D.R., Nelson K., Saunders R.D.C., Scheeler F., Shen H.,
RA Melson D.R., Welson K., Saunders R.D.C., Scheeler F., Shen H.,
RA Mennert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Mang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Mang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
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RN 121
                                                                                                                                                                                                                                                                                                         A Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,

Was Evans C.A., Gocsyne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,

Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,

A Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

Was Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

Was Carlson M., Center A., Champe M., Davenport L.B., Dietz S.M.,

Was Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

Was Carlson J.W., Center A., Champe M., Doyle C., Dresnek D., Farfan D.,

Was Carlson J.W., Center J. Hoskins R.A., Hostin D., Howland T.J.,

Was Carlson M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,

Was Carlson C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,

Was Carlson C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,

Was McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,

Was Pacleb J., Paragas W., Park S., Patel S., Pictifer B.,

Was Phousnenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,

Was Milliams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.,

"Sequencing of Drosophila melanogaster genome.",

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                         Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu I., Campbell Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D. Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris I Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E "Annotation of Drosophila melanogaster genome.";

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
SEQUENCE
                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20196006;
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FROM
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N.A
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ex S.E.,
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Best Local 9
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pfam; pF00052; laminin_B; 3.

pfam; pF00053; laminin_EGF; 2.

pfam; pF00054; laminin_G; 3.

pfam; pF00057; ldl_recept_a; 2.

pfam; pF00057; ldl_recept_a; 2.0

prints; pR00180; ldplracEFTOR.

SMART; SM00180; lGF_lam; 9.

SMART; SM00409; IG; 12.

SMART; SM00280; lami; 3.

SMART; SM00282; Lami; 3.

SMART; SM00192; LDIa; 23.
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InterPro; IPR001525; CS DNA meth.
InterPro; IPR008985; ConA like_lr
InterPro; IPR000742; EGF 2.
ITR000742; EGF 1ike.
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InterPro; IPR003599; I
InterPro; IPR007110; I
InterPro; IPR003598; I
InterPro; IPR0003598; I
InterPro; IPR002049; I
InterPro; IPR002049; I
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GO; GO:01
GO; GO:01
GO; GO:01
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Submitted
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SEQUENCE 4
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   3351
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GO:0003677; F:DNA binding;
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                                                                   170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E; PS00094; C5 MTASE 1; 1.

E; PS00022; EGF 1; 10.

E; PS00022; EGF 2; 6.

E; PS50116; EGF 2; 6.

E; PS501248; LAMININ TYPE EGF; 7

E; PS50025; LAM G DOWAIN; 3.

E; PS50025; LAM G DOWAIN; 3.

E; PS50029; LDLRA 1; 20.

E; PS50029; LDLRA 2; 23.

E; PS50030; RRM RNP 1; 1.

EjDobulin domain; Laminin EGF-li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                               SVSQLELQDSGTWTC
                                                                                                                                                                                                                                                                                                                     LWDQGNFPLIIKNLKIEDSDTYICEVED-----QKEEVQLLVFGLTA----NSDTHL---
VISNVSPSDAGNYVC
                                                                                                                               LPAKSRDYSLKLDDQSSNLRAGESTDVECYSSDDTYTDVVWERSDGAPLSNNVRQVGNRL
                                                                                                                                                                                            --LQGQSLTLTLESP----PGSSPSVQCRS---
                                                                                                                                                                                                                                                         -----ILVLTNLRPEDAGRYICNSYDVDRGQQLPEVSIDLQVLTATPPPNSPIYLPPQ
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MAR-2000) to the
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Ig_c2.
Laminin_B
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e EMBL/GenBank/DDBJ databases
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Pred. No. 1
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Mismatches
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RESULT 78
Q8MPN3
ID Q8MPN
AC Q8MPN

Q8MPN3;

PRELIMINARY;

PRT;

4223

B

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RA Adams N.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams N.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams N.D., Celniker S.E., Holt R.A., How., Hockins R.A., Galle R.F.,
RA George R.A., Lewis S E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S E., Richards S., Ashburner M., Henderson S.N.,
RA Button G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Barladon R.C., Rogers Y.H., Blazej R.G., Change M., Pfeiffer B.D.,
RA Barladon R.C., Rogers Y.H., Blazej R.G., Change M., Pfeiffer B.D.,
RA Barladon R.C., Rogers Y.H., Blazej R.G., Change M., Pfeiffer B.D.,
RA Barladon R.C., Rogers Y.H., Blazej R.G., Change M., Pfeiffer B.D.,
RA Barladon R.C., Rogers Y.H., Barwandale J., Bayraktaroglu L., Beasley E.M.,
RA Barlaw R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Bottlier P.,
RA Burtis K.C., Blasen D.A., Buller H., Gadleu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Dietz S.M.,
RA Gebabto B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Goldec C., Gabrellian A.E., Garg N.S., Gelbart W., Glasser K.,
RA Goldec C., Gabrellian A.E., Garg N.S., Gelbart W., Glasser K.,
RA Goldec C., Gabrellian A.E., Garg N.S., Gelbart W., Glasser K.,
RA Goldec C., Gabrellian A.E., Garg N.S., Gelbart W., Glasser K.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Klamel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Becleb J.M.,
RA Maris R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Dodson K., Dorsett V., Doup L.E., Doyle C., Dreenek D., Farfan D., Ferriera S., Friee E., Galle R.F., Garg N.S., George R.A., Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J., Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A., McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J., Paragas V., Park S., Patel S., Peiffer B., Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F., Stapleton M., Strong R., Svirskas R., Tector C., Tyler D., Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.; "Sequencing of Drosophila melanogaster genome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TROL OR EG:BACR25B3.11 OR CG7981.

Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
Celniker S.E., Adams M.D., Kronm
Evans C.A., Gocayne J.D., Amanat
Banzon J., An H., Baldwin D., Ba
Carlson J.W., Center A., Champe
Carlson J.W., Center A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Perlecan participates i Drosophila neuroblasts.' Submitted (MAY-2002) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2002 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
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Amanatides P.G., Brandon R.C., Rogers Y.,
D., Banzon J., Beeson K.Y., Busam D.A.,
Champe M., Davenport L.B., Dietz S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
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Best Local
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Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,
Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,
Searle S. M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.,
"Annotation of Drosophila melanogaster genome.";
[5]
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EMBL; AE
FlyBase;
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PROSITE;
PROSITE;
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                                                                                                                                                                                                                                                  SMART;
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PRINTS; PR00261; LDLRECEPTOR:
ProDom; PD003031; Laminin_B;
SMART; SM00180; EGF_Lam; B.
SMART; SM00409; IG; 13.
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Pfam; PF00053;
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InterPro;
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InterPro;
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GO; GO:0005198; F:structural molecu
GO; GO:0006306; P:DNA methylation;
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Celniker
                                                                                                                                                                                                                                          SMART;
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                               3237 REGENIQLOCTVTDQYGVRAQDNVEFNWFRDD
                                                                                                                                                                                                                                       ; SM00409; IG; 13.
; SM00408; IGc2; 13.
; SM00281; LamB; 3.
; SM00282; LamG; 3.
; SM00192; LDLa; 23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AJ487018; CAD31650.1; -. AE003424; AAN09079.1; -.
                                                                                                                                                                                                                                                                                                                                                                        PF00047;
86 LWDQGNFPLIIKNLKIEDSDTYICEVED-----QKEEVQLLVFGLTA----NSDTHL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.D., CEIL-
ted (MAR-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    e; FBgn0001402; trol.:
:0003677; F:DNA binding;
                                                                          45;
                                                                                                                                                3; PS00094; C5 MTASE 1; 1.

3; PS00022; EGF 1; 10.

3; PS01186; EGF 2; 6.

3; PS50185; IG LIKE; 12.

3; PS501248; LAMININ TYPE EGF 12.

5; PS01248; LAMININ TYPE EGF 12.

5; PS01209; LDLRA 1; 20.

5; PS50068; LDLRA 2; 23.

5; PS50068; LDLRA 2; 23.

5; PS50068; LDLRA 2; 23.
                                                                                                                                 lobu
                                                                                      Similarity
                                                                                                                                       PS00030; RRM_RNP_1; 1.
                                                 KKGDTVELTCTASQ-----KKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR001525; C5_DNA meth.
IPR008985; ConA_like_lec_gl.
IPR000742; EGF_2.
IPR006209; EGF_like.
                                                                                                                                                                                                                                                                                                                                                                                    IPR000504;
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                                                                                                                      4223
                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                            laminin_B; 3.
                                                                                                                   ΑA;
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                                                                                                                                                                                                                                                                        IGc2; 13.
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LDL_receptor_A.
RNA_rec_mot.
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Laminin_B.
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                                                                                                                      466919 MW;
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e EMBL/GenBank/DDBJ
                                                                         31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL/GenBank/DDBJ databases
                                                                        Score 118; DB
Pred. No. 1.3;
%1; Mismatches
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                                                                                                                                                                                    EGF;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             activity;
                                                                                      .3;
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                                                                                               Length 4223;
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RESULT 79

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                                                                                                                                                                                                                                                                                                                                             IBOId=Q23551-1; Sequence=External;
Note=No experimental confirmation available;
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEMBL; Z73899; CAA98064.1; --
EMBL; Z73899; CAA98064.1; JOINED.
EMBL; Z73899; CAA98081.1; --
EMBL; Z73897; CAA98081.1; --
EMBL; Z73897; CAA98081.1; --
EMBL; Z73897; CAA98081.1; --
EMBL; Z73897; CAA98081.1; --
EMBL; X15423; CAA93463.1; --
EMBL; X15423; CAA33463.1; --
EMBL; X15423; CAA33463.1; --
EMBL; X57242; S57242.
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Q23550, Q23020; Q27232;
01-NOV-1996 (TrEMBLrel. 06
01-NOV-1998 (TrEMBLrel. 06
01-OCT-2003 (TrEMBLrel. 25
                                                       GO; GO:0006468; P:protein amino acid InterPro; IPRO03962; FNIII subd. InterPro; IPR003961; FN_III. InterPro; IPR003957; FN_III-like. InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=93387664; PubMed=8397135; Benian G.M., L'Hernault S.W., Morri "Additional Bequence complexity in encoded protein, twitchin, of Caeno Genetics 134:1097-1104(1993).
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MEDLINE=90044042; PubMed=2812002;

Benian G.M., Kiff J.E., Neckelmann N., M
"Sequence of an unusually large protein
myosin activity in C. elegans.";

Nature 342:45-50(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. White S., Harris B.; Submitted (NOV-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UNC-22 protein.
UNC-22 OR ZK617.1.
Caenorhabditis elegans.
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                                                                                                                                                                                        GO:0005524; F:ATP binding; IEA.
GO:0004674; F:protein serine/threonine kinase
GO:0016740; F:transferase activity; IEA.
GO:0004811; F:tRNA ligase activity; IEA.
GO:0006418; P:amino acid activation; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=b;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=Q23550-1; Sequence=Displayed, Note=No experimental confirmation a
; IPR003961; FN_III_like.

IPR008957; FN_III_like.

; IPR00711; Ig_like.

; IPR003598; Ig_c2.

; IPR000719; Prot_kinase.
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exity in the muscle gene, unc
of Caenorhabditis elegans.";
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                                                                                                                                                               phosphorylation;
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n implicated in
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Best Local S
Matches 58
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SMART; SM00408; IGC2; 6.

SMART; SM00408; IGC2; 6.

SMART; SM00220; STKc; 1.

PROSITE; SM00220; STKC; 1.

PROSITE; PS00118; AA TRNA LIGASE I; 1.

PROSITE; PS00107; PROTEIN KINASE ATP; 1.

PROSITE; PS00107; PROTEIN KINASE DOM; 1.

PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

SEQUENCE 6831 AA; 752596 MW; 6CADE032963A52E1

SEQUENCE 6831 AA; 752596 MW; 6CADE032963A52E1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q23551;
Q23551;
01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TrEMBLrel. 01, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein ZK617.1b (C. elegans UNC-22 pro
(Corresponding sequence ZK617.1b).
ZK617.1B OR UNC-22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00041; fn3; 31.
Pfam; PF00047; ig; 21.
Pfam; PF00069; pkinase; 1.
                                          White's.
                                                                                                                                                                                 "Genome sequence of the neminvestigating biology.";
Science 282:2012-2018(1998)
                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=Bristol N2;
MEDLINE=99069613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rhabditidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Nematoda; Chromadorea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PRO0014; FNTYPEIII.
ProDom; PD000001; Prot kina
SMART; SM00060; FN3; 27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR008271; Ser_thr_pkin_AS
InterPro; IPR001412; tRNA-synt_I.
                                                                         STRAIN-Bristol
                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80
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58; Conser
                                                                         FROM N.A.
bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGSALPDPQ 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FIVALKDTEVIEKDDVTLMCQTKDTKTPGIWFRN--GKQISSMPGGKFETQSRNGTHTLK 1135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RHTFVV----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -LTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQ---
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   (MAY-1996)
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                                                                                                                                                                                                                                                                                                                                       PubMed=9851916;
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the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                              nematode
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Pred. No. 2.5;
36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -KV---NESDLATLETDVNDKDAEVVWWHDGKRIDIDGVK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTWTCTVLQNQ------KKVEFKIDIVPRASALPAPP
                                                                                                                                                                                                                                                              C.elegans: A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rhabditida;
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                                                                                                                                                                                                                                                              platform
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rhabditoidea;
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DR PDB; 1WIT; 23-DEC-96.

DR PDB; 1WIT; 23-DEC-96.

DR PDB; 1WIT; 23-DEC-96.

DR PDB; 1WIU; 23-DEC-96.

DR GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0004674; F:protein-tyrosine kinase activity; IEA.

DR GO; GO:00046713; F:protein-tyrosine kinase activity; IEA.

DR GO; GO:0004618; P:protein-tyrosine kinase activity; IEA.

DR GO; GO:0006418; P:protein-tyrosine kinase activity; IEA.

DR GO; GO:0006418; P:protein amino acid phosphorylation; IEA.

DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

DR InterPro; IPR003961; FNIII subd.

DR InterPro; IPR003961; FNIII subd.

DR InterPro; IPR003961; FNIII-like.

DR InterPro; IPR003961; FNIII-like.

DR InterPro; IPR003599; IG-2.

DR Pfam; PF00047; IG; 21.

DR Pfam; PF00049; IG; 30.

DR SMART; SM00408; IGC2; 24.

DR PROSITE; PS00179; PATEIN KINASE DOM; 1.

DR PROSITE; PS00179; PATEIN KINASE DOM; 1.

DR PROSITE; PS00179; PATEIN KINASE DOM; 1.

DR PROSITE; PS00179; PATEIN KINASE ST; 1.

DR PROSITE; PS00179; PATEIN KINASE ST; 1.

DR PROSITE; PS00179; PATEIN KINASE ST; 1.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical SEQUENCE 7
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                                                                                                                                                                                                                                                            1313
1522
                                                              1463
                                                                                                                               1405
                                                                                                                                                                                             1360
                                                                                              171
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                                                                                                                                                                                                                                                                                           RHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGS
KGTRRGDPK 1530
                                                                                              VSQLELQDS------GTWTCTVLQNQ-----KKVEFKIDIVPRASALPAPP 210
                                                                                                                               FIVALKDTEVIEKDDVTLMCQTKDTKTPGIWFRN-
                                                                                                                                                                                                                            FLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFG---
                                                                                                                                                                                                                                                            RHTFVV-----PMKSQ--KV---NESDLATLETDVNDKDAEVVWWHDGKRIDIDGVK--
                              TGSALPDPQ
                                                              IGKIEMNEADVYEIDOAGLRGSCNVTVLEAEKRPILNWKPKKIEAKAG-EPCVVKVPFQI
                                                                                                                                                           -LTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQ---GGK-----
                                                                                                                                                                                               ----FKVESSNRKRR---
                                                                                                                                                                                                                                                                                                                                                                                        nl protein.
7158 AA;
                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                        9.0%;
                              219
                                                                                                                                                                                                                                                                                                                                                                                         788947 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOINED.
                                                                                                                                                                                                                                                                                                                           36;
                                                                                                                                                                                                                                                                                                                         Score 118; DB Pred. No. 2.7; 36; Mismatches
                                                                                                                                                                                            -----LIINGARIEDHGEYKCTTKDDRTMAQLIVDAKNK 1404
                                                                                                                                                                                                                                                                                                                                                                                         561EF9DB13387505 CRC64;
                                                                                                                                                                                                                                                                                                                                       DB 5; Length 7158;
                                                                                                                             -GKQISSMPGGKFETQSRNGTHTLK
                                                                                                                                                                                                                                                                                                                           87;
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                                                                                                                                                                                                                                                                                                                           68;
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RESULT
Q9VNP2
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Best Local S
Matches 55
                                                                     Q9VNP2
Q9VNP2;
Q9VNP2;
01-MAY-2000 (TrEN
01-OCT-2002 (TrEN
01-OCT-2003 (TrEN
CG8779 protein.
NRM OR CG8779;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               002869;
002869;
01-JUL-1997
01-JUL-1997
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eur. J. Neurosci. 9:1105-1116
EMBL; Z94719; CAB08114.1; -.
PIR; JC5519; JC5519;
InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig_c2.
                                 Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Ins.
Neoptera; Endopterygota; Diptera; Brachycera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00047; ig; 3.
SMART; SM00408; IGc2; 2.
PROSITE; PS50835; IG_LIKE; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bruemmendorf T., Spaltmann F., Treubert U.; "Cloning and characterization of a neural cell recognition axons of the retinotectal system and spinal cord."; Eur. J. Neurosci. 9:1105-1116(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chiamp, gli-isoform precursor.
        Ephydroidea; Drosophilidae;
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brain; GPI-anchor; Immunoglobulin domain; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=97358596; PubMed=9215692;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                            243
                                                                                                                                                                                                                                   205
                                                                                                                                                                                                                                                          183
                                                                                                                                                                                                                                                                                   170
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                                                                                                                                                                                                                                                                                                                                                                               62 LGNQGSFLTKGPSKLNDRAD-SRRSLWDQGNFPLIIKNLKIEDSDTYICEYEDQ----KE
                                                                                                                                                                                                                                                                                                                                                                                                          14
                                                                                                                                                                                                                                                                                                                                                                                                                               10 LILVIQIALLPAA-----TQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                           AVPTP
                                                                                                                                                                                                                                   ALPAP
                                                                                                                                                                                                                                                          EILGITREQSGKYECKAANEVASADVKQVRVTVNYPPTITESKSNEAATGRQALLRCEAS
                                                                                                                                                                                                                                                                                 SVSQLELQDSGTWTCTVLQ-----NQKKVEFKIDIVP-----
                                                                                                                                                                                                                                                                                                           QVYLIVQVPPKISNISSDITVNEGSNVTLVCMANGRPEPVITWRHLTPTGKEFEGEEEYL
                                                                                                                                                                                                                                                                                                                                 EVOLLVFG----LTANSDTHLLQGQSLTLTLESPPGSSPSVQCR--SPRGKNIQGGKT-L
                                                                                                                                                                                                                                                                                                                                                         AG-----EDKWSLDPRVELEKRSPLE---YSLRIQKVDVYDEGSYTCSVQTQHHPKTS
                                                                                                                                                                                                                                                                                                                                                                                                        LVLLRLLCLLPTGLPVRSVDFTRGTDNITVRQGDTAILRCFVEDRSS-KVAWLNRSGIIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29
350 AA;
                                                                                             (TrEMBLrel. 13, (TrEMBLrel. 22, )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel. 04, (TrEMBLrel. 04, (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                           247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation updat
                                                                                               Last
Last
                       Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 117;
Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
CHLAMP, G11-ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0844A892878894D4 CRC64;
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                                                                                              sequence update) annotation updat
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                                              Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         93;
                                   Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    molecule
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                                                                                                                                                                                                                                                                                    ----RAS
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Adams D., Celniker S.E., Hilt R.A., Evans C.A., Gocayne J.D.,
RA Adams D., Celniker S.E., Hilt R.A., H., Hothins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Barlaw R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Becker R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Berkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Glerry J.M., Cawley S., Dahlke C., Davapport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davapport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davapport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Cherry J.M., Cawley S., Dahlke C., Davapport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Pleischmann W.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Mattei B., McIntosh T.C., McLeod M., H., Ibegvam C.,
RA Liuk N., Mattei B., McIntosh T.C., McLeod M., H., Ibegvam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D. Lai Z.,
Liang Y., Lin X.,
RA Merkilov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nelson K., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Melson D.R., Nelson K., Saunders R.D.C., Scheeler F., Shen H.,
RA Mount S.M., Modra G.S., Fan S., Pollard J., Puri V., Reese M.G.,
RA Maris M., Wenter J.S., Zhan M., Zhang G., Zhao Q., Zheng Y.,
RA Shue B.C., Stapleton M., Skupski M.P., Smith T.,
RA Shue B.C., Stapleton M., Shupski M.P., Smith T.,
RA Shue B.C., Stapleton M., Zhang G., Zhao Q., Zheng L.,
The Global R.L., Smith H.O.,
The Global R.L., Smith H.O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Banzon J.W., Gocayne J.D., A
Banzon J.W., An H., Baldwin D
Carlson J.W., Center A., Ch
Dodson K., Dorsett V., Doup
Ferriera S
                                                                     Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,
Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,
Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,
Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
"Annotation of Drosophila melanogaster genome.";
Submitted (MAR-2000) to the EMBL/Gennamy/nnc...";
                                                                                                                                                                                                                                                                                                                           Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M., Dodson K., Dorsett V., Doup L.B., Doyle C., Dreenek D., Farfan D., Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A., Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J., Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A., McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J., Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B., Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F., Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.; "Sequencing of Drosophila melanogaster genome."; "Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
SEQUENCE FROM N.A.
Adams M.D., Celniker
Submitted (MAR-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-20196006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FROM N.A.
S.E., Adams
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              M. U.
S.E., C
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Gibbs R.A., Rubin G.M., Vento
e EMBL/GenBank/DDBJ databases
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                       Venter
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Best Local S
Matches 48
             PIR; T13669; LISUUJ:
FlyBase; FBgn0005629; nrm.
GO; GO:0005886; C:plasma membrane; I:
InterPro; IPR003599; IG.
InterPro; IPR007110; Ig-like.
Pfam; PF00047; Ig; 8.
SMART; SM00409; IG; 5.
PROSITE; PS50835; IG_LIKE; 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR002086; Aldehyde_dehydr.
InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003598; Ig_c2.
InterPro; IPR0047; ig; 6.
SMART; SM00409; IG; 5.
SMART; SM00408; IGc2; 4.
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  SEQUENCE
                                                                                                     EMBL; L23146; AAA03750.1; PIR; T13669; T13669.
                                                                                                                                    MEDLINE=94000831; PubMed=8398154; Kania A., Han P.L., Kim Y.T., Bell Kania A., Han P.L., Kim Y.T., Bell Warromusculin, a Drosophila gene precursors and muscles, encodes a
                                                                                                                                                                                                        NCBI_TaxID=7227;
                                                                                                                                                                                                                   Eukaryota; Metazoa; Arthropoda; Hexapoda; Inso
Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                     Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                              Q24273;
01-NOV-1996
                                                                                                                                                                                                                                                                                                                                      Q24273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; PROSITE; PS50835; IG_LIKE; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FlyBase; FBgn0005629; nrm.
GO; GO:0005886; C:plasma membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted
                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                   NRM OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE003599;
                                                                                                                         Neuron 11:673-687 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunoglobulin
                                                                                                                                                                                                                                                                                                                                                            83
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                                                                                                                                                                                                                                                                                                                                                                                              183
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                                                                                                                                                                                                                                                                   CG8779.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               l Similarity
48; Conserv
                                                                                                                                                                                                                                                                                                                                                                                             TCTVLQNQKKVE
                                                                                                                                                                                                                                                                                                                                                                                                                                          FFIPEETCDN-FNGYRIELRVLVPP---TEVVILDAKGDRIKNGSV--VGPMQERQSLKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                               FGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GD-----SNVTSVNKEFDERVTV-EQNPYRLVIKDLKIADEDIYLCDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLV 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LVLVLCLALVDSSTAQVDTTISQQESQSVVLPCPVDAEKCGKLHSLNWFKGDDRIAAMLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLLVLQLALLPAAT-QGNKVVLGKKGDTVELTCTASQKKSIQFH----WKNSNQI--KIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SEP-2002)
  1011 AA;
                                                                                                                                                                                                                                                                                       (TrEMBLrel.
                                                                                                                                                                                                                                                                                                              (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90442 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8.9%;
  113125 MW;
                                                                                                                                                                                                                                                                                       01,
01,
25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38;
                                                                                                                                                                                                                                                                                       Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 117; DB 5
Pred. No. 0.19;
38; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL/GenBank/DDBJ databases.
                                                                                                                                                            Bellen H.;
                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BAC689EA2C8E23F4 CRC64;
  AFD8A2A015D3AE63 CRC64;
                                                                                                                                       expressed in peripheral neuronal cell adhesion molecule.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IDA.
                                                                                                                                                                                                                                           Insecta;
                                                                                                                                                                                                                                                                                                    update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                          Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                182
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RESULT
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                                                                                                                                                                                                                                                                                                                                              RC STRAIN-C57BL/GJ; TISSUE-Blastocyst;

X MEDLINE-22388257; PubMed=12477932;

X MEDLINE-22388257; PubMed=12477932;

X MEDLINE-22388257; PubMed=12477932;

X MIT STRAIN-C57BL/GJ; TISSUE-Blastocyst;

X Mit Strausberg R.L., Feingold E.A., Grouse L.H., Darge J.G.,

X Mit Strausberg R.L., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,

X Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

X Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

X Altschul S.F., Zeeberg B., Buetow K.H., Wang J., Hong L.,

X Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,

X Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,

X Altschul S.F., Jordan H., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

X Altschul S.F., Loguellano N.B., Foers G.J., Abramson R.D., Mullahy S.J.,

X Altschul S.F., Loguellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

X Altschul S.F., Moorley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

X Allalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

X Allalon D.K., Moorley K.C., Shevchenko Y., Bouffard G.G.,

X Hilling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

X Hilling M., Madan A., Young A.C., Shevchenko Y., Butterfield Y.S.,

X Toros S. T. Marra M. A., Schmutz J., Myers R.M., Butterfield Y.S.,

X Toros S. T. Marra M. A., Schmutz J., Myers R.M., Schein J.E.,

X Toros S. T. Marra M. A., Schmutz J., Schmerch A., Schein J.E.,
                                                                  Query Match
Best Local S
Matches 62
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q7TQ03;
                                                                                                                                       Hypothetical protein. SEQUENCE 192 AA; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein.
                                                                                                                                                                        Submitted (MAY-2003) to the EMBL; BC052651; AAH52651.1;
                                                                                                                                                                                                         Strausberg R.;
                                                                                                                                                                                                                                                                                              Jones S.J., Marra M.A.;
"Generation and initial analysis
and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                            STRAIN=C57BL/6J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84
                                                                                                                                                                                                                                                QUENCE
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σ
                                                                   Similarity
62; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LVLVLCLALVDSSTAQVDTTISQQESQSVVLPCPVDAEKCGKLHSLNWFKGDDRIAAMLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLLVLQLALLPAAT-QGNKVVLGKKGDTVELTCTASQKKSIQFH----WKNSNQI--KIL
                               LLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQF-HWKNSNQIKILGNQGSF
                                                                                                                                                                                                                                                FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTW
 VLLSTFLLLLPAASGAFQEVHGTGGDPVTLPCSYPESRILSFVCWGRGECASDTCGQTLV 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCTVRNTRPQPE 194
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(TrEMBLrel. 25, Last seq
(TrEMBLrel. 25, Last ann
                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                              TISSUE=Blastocyst;
                                                                                                                                                                                                                                                                                   Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                         20905 MW;
                                                                                  8.8%;
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                                                                   19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 117; DB
Pred. No. 0.25
38; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                             EMBL/GenBank/DDBJ databases
                                                                  Score 116.5; DB
Pred. No. 0.032;
9; Mismatches
                                                                                                                                       E4213FCE00540D7F CRC64;
                                                                                                                                                                                                                                                                                                                    of more than 15,000
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                                                                                                    DB 11; Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76;
                                                                     82;
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                                                                     Indels
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                                                                                                        192;
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                                                                   Gaps
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O43 608
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O40
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D7 01
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C6 04
C7 04
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C7 07
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Best Local S
Matches 58
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O43608;
O1-JUN-1998
O1-JUN-1998
O1-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunoglobulin on NON_TER 185 NON_TER 285 SEQUENCE 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDITINE-98117249; PubMed=9458045; Kidd T., Brose K., Mitchell K.J., Fetter R.D., Tessier Goodman C.S., Tear G.; Goodman C.S., Tear G.; Tear G.; Tessing of the CNS midline novel subfamily of evolutionarily conserved guidance r Cell 92:205-215(1998).

EMBL, AF040991; AAC39576.1; -.

GO; GO:000046; F:axon guidance receptor activity; NAS GO; GO:0007417; P:central nervous system development;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003951; FN_III.
InterPro; IPR008957; FN_III-like.
InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig_c2.
Pfam; PF00041; fn3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Roundabout 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85
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                                           164
                                                                                       182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126
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                                                                                                                                                                                                                              54 -LTITNIQRSDAGYYICQA--
                                                                                                                                                                                                                                                                            93
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                                                                                                                                                                                                                                                                                                                          v
                                                                                                                                                                                                                                                                                                                                                                                                                 h 8.8%; Score 116.5; DB Similarity 22.8%; Pred. No. 0.053; Similarity 27.8%; Pred. No. 0.053; Mismatches
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PPAASALPAALAVI 240
                                                                                       WTCTVLQNQKKVEFK--IDIVPRA--
                                                                                                                                                                                     SSPSV-----QC-----
                                                                                                                                                                                                                                                                     PLIIKNLKIEDSDTYICEVEDQKEEVQLLVFG-LTANSD---THLLQGQSLTLTLESPPG
                                                                                                                                                                                                                                                                                                                                                                        KGDTVELTCTASOKKSIOFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNF
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                                                                                                                                     QTLAVDGTALLKCKATGDPLPVISWLKEGFTFPGRDPRA-TIQEQGTLQIKNLRISDTGT
                                                                                                                                                                                                                                                                                                                        QGRTVTFPCETKGNPQPAVFWQKE-----GSQNLLFPNQPQQPN----SRCSVSPTGD-
                                         YTCVATSSSGEASWSAVLDVTESGATISKNYDLSDLPGPPSKPQVTDVTKNSVTLSWQPG
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285 ]
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(TrEMBLrel.
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; 30606 MW;
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Primates;
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25,
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Last annotation updat
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Catarrhini;
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                                                                                                                                                                                                                                   -----LTVAGSILAKAQLEVTDVLTDRPPPIILQGPAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05DF916A3DBA96C6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --RPEPPSLVAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g of the CNS midline and defines conserved guidance receptors.";
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                                                                                                                                                                                     ----RSPRGKNIQGGKTLSVSQLELQDSGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vertebrata; Euteleostomi;
                                                                                         --SALPAPPTGSALPD----PQTASALPD
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Champe M., Chavez C., Dorsett V., Farfan D., Frise E., Get Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungal RA Nunco J., Pacaleb J., Paragas V., Park S., Phouanenavong S. RA Yu C., Lewis S.E., Rubin G.M., Celniker S.; RL Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases. PRE EMBL; AE003822; AAR593253.1; -. RHSSP; P56276; 1TLK.
                  RX MEDLINES-2019606; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,
RA Amanatidee P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Adams M.D., Cangers Y.H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Baradon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Baradon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Ballew R.M., Bayari A., An H.-J., Andrews Pfannkoch C. Bassley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Bartis R.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Dolshakov S.M.,
Dodson K., Doup L.E., Downes M., Dugan Roccha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Bvangelista C.C., Ferraz C., Ferriera S., Pleischmann W.,
RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Netchum K.A.,
RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Nebrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Noy M., Murphy B., Murphy L., Muzzy D.M., Nelson D.L.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Hold B.E., Siden-Kiamos I., Simpson M., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Suppski M.P., Smith T.,
RA Shue B.C., Stapleton M., Strong R., Sun E.,
RA Spier E., Spradling A.C., Scapleton M., Strong R., Sun E.,
RA Herry Y.Ph R.-F., Zavert J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
The genome sequence of Drosophila melanogaster.",

RA Spier J. Shan M., Shou K., Smith H.O.,
RA Spier S. Shan M., Schola R., Shith H.O.,
RA Shen B. Shan R., Robing R., Shith H.O.,
RA Shen B. Shan R., Shith G.M., Venter T.,
Ra Sh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-Berkeley;
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25,
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                                                                                                                               L., Agbayani A., Carlson J.,
Farfan D., Frise E., George
iao G., Miranda A., Mungall C.
Park S., Phouanenavong S., Wa
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                                                                                Pfam; PF00041; fn3; 
Pfam; PF00047; i9; 3
PRINTS; SM00016; FN3;
SMART; SM00060; FN3;
SMART; SM00409; IG;
SMART; SM00408; IGc2
SMART; SM00406; IGv2
SMART; SM
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InterPro; IPR003598; Ig_c2.
Pfam; PF00047; ig; 3.
SMART; SM00408; IGc2; 2.
PR0SITE; PS50835; IG_LIKE; 3
Immunoglobulin domain.
SEQUENCE 359 AA; 39939 MM
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Q8NCE6;
01-OCT-2002
01-OCT-2002
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                                                                                                                                                                                                                                                                                                                                                                                SMDMITCEG (Mar. 2007).

EMBL; AKO74780; BACCII205.1; —

InterPro; IPR003962; FAIII subd.

InterPro; IPR003961; FN_III.

InterPro; IPR008957; FN_III-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                            InterPro; IPR008957;
InterPro; IPR003599;
InterPro; IPR007110;
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                                                                                                                                                                                                                                                                                             InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003596; Ig_v.
Deam. BERGOA1. fn2. 3
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                      Local
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                                                                                I; SM00060; FN3; 3.
I; SM00409; IG; 2.
I; SM00406; IGv; 2.
I; SM00406; IGv; 2.
IT; SM00406; IGv; 2.
IT; PS50835; IG_LIKE; 2.
ENCE 570 AA; 62110 MW; 45CEBDBH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47;
. Similarity 58; Conserv
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(TrEMBLrel. 22, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
(protein FLJ90299.
(Human).
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                                                                                                                                                                                                                                       FNTYPEIII.
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                    8.8%;
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Ig_c2.
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                      Pred.
                                          Score 116.5;
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Pred. No. 0.
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                                                                                   bulin domain; Repeat.
45CEBDBB5B340195 CRC64;
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                      13;
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                                          Length 570;
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; Homo.
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Saito K.,
shari K.,
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Q865F2;
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Q7Z681;
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DKFZP779D0163.
Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                Q865F2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fobo G., Han M., Wiemann S.;
Submitted (JUN-2003) to the
EMBL; BX537757; CAD97826.1;
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01-OCT-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical
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52; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WTCTVLQNQKKVEFK--IDIVPRA--
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                                                                                                                                                                                                                        RARDEGSYTCSAYQGSQAVSRSTEVKV-VSPAPTAQPKDPGRDCVDQPELAN
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                                                                                                                                                                                                                                                                                                                      VTV--PEGDTARLLCVVAGESVNIRWSRNGLPVQADGHRVHQSPDG-----TLLIYNL
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(TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel. 25, Created)
(TrEMBLrel. 25, Last sequence update)
(TrEMBLrel. 25, Last annotation updat
(protein DKFZp779D0163 (Fragment).
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larity 22.4%;
Conservative 2
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                                                Created)
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Pred. No. 0.16;
9; Mismatches
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sequence update) annotation updat
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Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam, PF00047; ig; 5.

PRINTS; PR01472; ICAMVCAM1.

PRINTS; PR01474; VCAM1.

SMART; SM00409; IG; 5.

SMART; SM00409; IGc2; 5.

PROSITE; PS50835; IG LIKE; 5.

SEQUENCE 739 AA; 81806 MW;
                                                                                                                                                                                                                  Hypothetical protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Ch
Mammalia; Eutheria; Pr
Rowen L., Madan A., Qin S., Abbasi N., Dors M. Madan A.; Dickhoff R., Shaffer T., James R., I "Complete sequence of the gene for presenting submitted (NOV-1998) to the EMBL/GenBank/DDBJ EMBL; AF109907; AAC97963.1; -. HSSP; P12111; ZKNT. GO; GO:0004867; F. serine protease inhibitor ac InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Modulation of basal and interleukin-1-induced adhesion molecule expression by phospholipid hydroperoxide glutathione peroxidase 15-lipoxygenase in rabbit aortic smooth muscle cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schnurr K., Banning
Brigelius-Flohe R.,
                                                                                                                                                                                                                                                                                                  01-MAY-1999
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota;
Mammalia; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                        01-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A
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                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32 KKGDTVELTCTASOKKSIOFHWKNSNOIKILGNOGSFLTKGPSKLNDRADSRRSLWDQGN
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                                                                                                                                                                                                                                                                                              (TrEMBLrel. 10, (TrEMBLrel. 10, ) (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Banning
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                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                      Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lagomorpha; Leporidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.8%; Score 116.5; D
21.9%; Pred. No. 0.18;
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                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                            PRT;
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                                                                                                                                          Dors M.,
                                                                                                                        R., Lasky S., Hoo
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                          activity;
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RESULT 91
Q9HCK4
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Best Local S
Matches 52
InterPro; IPR007110; 15
InterPro; IPR003598; Ig_c2.
InterPro; IPR003598; Ig_c2.
Pfam; PF00041; fn3; 3.
Pfam; PF00047; 19; 5.
SMART; SM00060; FN3; 3.
SMART; SM00408; IGc2; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ProDom; PD000222; Kunitz BPTI; 1.
SMART; SM00408; IGC2; 3.
SMART; SM00131; KU; 1.
SMART; SM00131; KU; 1.
SMART; SM00209; TSP1; 5.
PROSITE; PS00280; BPTI KUNITZ 1; 1
PROSITE; PS50279; BPTI KUNITZ 2; 1
PROSITE; PS50279; BPTI KUNITZ 2; 1
PROSITE; PS50379; GTIKE; 3.
PROSITE; PS50092; TSP1; 5.
Hypothetical protein; Immunoglobul.
                                                                      EMBL; AB046788; BAB13394.1; -.
HSSP; PS6276; ITLK.
Genew; HGNC:10250; ROB02.
InterPro; IPR003961; FN III.
InterPro; IPR003957; FN III-like.
InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig-C2.
Dfam: BR00411 fp3. 3
                                                                                                                                                                                                                                                                                                                                                 01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein KIAA1568 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
InterPro;
                                                                                                                                                                       MEDILINE-20450683; PubMed=10997877;
Nagase T., Kikuno R., Nakayama M., Hirosawa M., Ohara O.;
"Prediction of the coding sequences of unidentified human
XVIII. The complete sequences of 100 new cDNA clones from
code for large proteins in vitro.";
DNA Res. 7:273-281(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00047; ig; 3.
Pfam; PF00014; Kunitz_BPTI;
Pfam; PF00090; tsp_1; 5.
PRINTS; PR00759; BASICPTASE.
                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Serine protease
SEQUENCE 1235
                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                             Q9HCK4;
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                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                           KIAA1568.
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52; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VTV--PEGDTARLLCVVAGESVNIRWSRNGLPVQADGHRVHQSPDG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LTLESPPGSSPSVQC----
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IPR002223; Kunitz_BPTI.
IPR000884; TSP1
                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 116.5;
Pred. No. 0.3
                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                            Query Match
Best Local S
Matches 52
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01-OCT-2002
01-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nishi T., Ota T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S. Yamamoto J., Isono Y., Kawai-Hiu Y., Saito K., Nishikawa T., Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M., Murakawa K., Kanehori K., Kikuchi H., Kanda K., Wagatsuma A., Sugiyama A., Kawakami B., Suzuki Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B., Suzuki Sugano S., Nagai K., Masuho Y., Nagai K., Isogai T.; "NEDO human cDNA sequencing project."; Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases. EMBL, AK092307; BAC03858.1; -
                                                                                                                                                                                                                                          Pfam; PF00047; ig; 3.

SMART; SM00409; IG; 3.

SMART; SM00408; IGc2; 3.

PROSITE; PS50835; IG_LIKE; 3.

Hypothetical protein; Immunoglobulin
Hypothetical protein; Jamuanoglobulin
SEQUENCE 354 AA; 38779 MW; 5DC938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation updat
Hypothetical protein FLJ34988.
Homo sapiens (Human).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrat.
Mammalia; Eutheria; Primates; Catarrhini; Hominid
                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like
InterPro; IPR003598; Ig_c2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Brain;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
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LNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTA--
                                                PWAAVDNMMV--RKGDTAVLRCYLEDGAS-KGAWLNRSSIIFAG--GDKWSVDPRVSIST
                                                                                           PAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGP----SK
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                                                                                                                                              Conservative
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                                                                                                                                            Score 116; DB 4;
Pred. No. 0.078;
6; Mismatches 94
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Catarrhini; Hominidae
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Q7TPD3;
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PROSITE; PS00290; IG MHC; 2.
Hypothetical protein.
SEQUENCE 484 AA; 52567 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; BC003495; AAH03495.1;
PIR; F33932; F33932.
HSSP; P01810; 2FBJ.
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Mammalia; Eutheria; Rodentia;
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SMART; SM00406; IGv; 1.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VLQLALLPAATQGNKV------VLGKKGDTVELTCTASQKKSIQF--HWKNSNQIKI
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                                                                                                                                                                                                                                                         -ELDV---NCSGPTPPPPITIPSCQPSLSLQRP-----ALEDLLLGSDASITCTL
                                                                                                                                                                                                                                                                                                                                                                      GTMNVTWGKSGKDITTVNFPPALASGGRYTMSSQLTLPAVECPEGESVKCSVQHDSNPVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VQLLVFGLTANSDTHLLQGQSLTLTLES------PPGSS-----
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     (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----DYWGQGTSVTVSSESARNPTIYPLTLPPALSSDPVIIGCLIHDYFPS
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Last annotation update)
                                                            Created)
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Q9VY33 PRELIMINARY; PRT; 344 F
Q9VY33; Q95SR2;
01-MAY-2000 (TYEMBLrel. 13, Created)
01-QCT-2002 (TYEMBLrel. 22, Last sequence
01-QCT-2003 (TYEMBLrel. 25, Last annotation
CG32600 protein (GH05565p).
CG32600 QR CG5291 QR CG11477 OR CG14415.
Drosophila melanogaster (Fruit fly).
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XX MEDLINE-273BL/6; TISSUE-Brain;
XX MEDLINE-22388257; PubMedel12477932;
XX MEDLINE-22388257; PubMedel12477932;
XX MEDLINE-22388257; PubMedel12477932;
XX MEDLINE-2388257; PubMedel12477932;
XX MILESCHUL S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
XX Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
XX Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
XX Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
XX Lapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
XX Stapleton M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,
XX Stapleton M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,
XX Stapleton M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,
XX Alphards S., Morley N.A., Peters G.J., Abramson R. D., Mullahy S.J.,
XX Alphards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
XX Alphards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
XX Alphards S., Worley C., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
XX Milalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
XX Alphards M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
XX Milalon D.K., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
XX Alphards M. J., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
XX Alphards M. J., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
XX Alphards M. J., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
XX Alphards M. J., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
XX Alphards M. J., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
XX Alphards M. J., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
XX Alphards M. J., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
XX Alphards M. J., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
XX Alphards M. J., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
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Best Local S
Matches 60
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Submitted (JUL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jones S.J., Marra M.A.; "Generation and initial analysis of and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                  PPAASALPAALAVI
                                                                                                                                                                                                WTCTVLQNQKKVEFK--IDIVPRASA-----
                                                                                                                                                                                                                                                                  QTLAVDGTALLKCKATGEPLPVISWLKEGFTFLGRDPRA-TIQDQGTLQIKNLRISDTGT
                                                                                                                                                                                                                                                                                                                                 QSL----TLTLESPPGSSP------SVQCRSPRGKNIQGGKTLSVSQLELQDSGT
                                                                                                                                                                                                                                                                                                                                                                                                   -LTITNIORSDAGYYICOA-----LTVAGSILAKAOLEVTDVLTDRPPPIILOGPIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PLIIKNLKIEDSDTYICEVEDQKEEVQLLVFG------LTANSDTHLLQG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QGRTVTFPCETKGNPQPAVFWQKE-----GSQNLLFPNQPQQPN----SRCSVSPTGD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNF
TP--GVLPASAYII
                                                                                                                                    YTCVATSSSGETSWSAVLDVTESGATISKNYDMNDLPGPPSKPQVTDVSKNSVTLSWQPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.8%; Score 115.5; D
23.6%; Pred. No. 0.26;
vative 28; Mismatches
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561
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Last sequence update) Last annotation updat

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RA Addms M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Addms M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Barlandon R.C., Rogers Y.-H.C., Blaze R.G., Champe M., Pfeiffer B.D.,
RA Barlandon R.C., Rogers Y.-H.C., Blaze R.G., Champe M., Pfeiffer B.D.,
RA Barlandon R.C., Rogers Y.-H.C., Blaze R.G., Champe M., Pfeiffer B.D.,
RA Barlandon R.C., Rogers Y.-H.C., Blaze R.G., Champe M., Pfeiffer B.D.,
RA Barlandon R.C., Barcar B.G., Helt G., Nelson C.R., Mikbos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Ffennkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L.D., Bessley E.M.,
RA Besson K.Y., Bence P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Gerbios B., Delcher A., Deng Z., Mays A.D., Dew I., D., Botchar I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Duvies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Duvies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Duvies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Duvies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Duvies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Duvies P.,
RA Geodson K., Doup L.E., Downes M., Dugan R., Dukov B.C., Dunn P.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Karpen G.H., Ke Z., Kemison J.A., Kechum N.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Degwam C.,
RA Hostin D., Houston K.A., Naon K., Neisenison J.A., Wesheri A.,
RA Hollin M., Kalluh F., G., Pan S., Pollard J., Puri V., Reese M.G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,

A Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,

A Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,

Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

A Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

A Carlson J.W., Center A., Champe M., Davenport L.B., Farfan D.,

Frise E., Galle R.F., Garg N.S., George R.A.,

Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,

A Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,

A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,

Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,

Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,

A Phouanenavong S., Pittman G.S., Smith H.O., Venter J.C., Rubin G.M.;

"Sequencing of Drosophila melanogaster genome.";

"Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbel Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D. Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E "Annotation of Drosophila melanogaster genome.";
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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InterPro; IPR007110; Ig-like.
InterPro; IPR007181 Ig_c2.
InterPro; IPR003598; Ig_c2.
Pfam; PF00047; ig; 2.
SMART; SM00408; IGc2; 2.
SMART; SM00408; IGc2; 2.
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                                                              Homo sapien
Eukaryota;
Mammalia; E
                                                                                                                           Q7Z3Y4
Q7Z3Y4;
01-OCT-2003
                                                 Mammalia; Eutheria;
NCBI_TaxID=9606;
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Champe M., Chavez C., Dorsett V., Farfan
Gonzalez M., Guarin H., Li P., Liao G.,
Nunoo J., Pacleb J., Paragas V., Park S.
Yu C., Lewis S.E., Rubin G.M., Celniker
TISSUE=Skeletal muscle;
MEDLINE=22388257; PubMe
Strausberg R.L., Feingo
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunoglobulin
SEQUENCE 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE003495; AAF48372.2; -. EMBL; AY060637; AAL28185.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yu C., Lewis S.E., Rubin G.M., Celniker S.; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases
                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FlyBase; FBgn0052600; CG32600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted
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                                                                                 sapiens (Human).
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.D., Celniker
ed (MAR-2000)
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                                                                                                                                                                                                                                                             GTWTCTVLQNQKKVEFKIDIV--PRASALPAPPTGSALPDPQTASALPDPPAASALPAAL
                                                                                                                                                                                                                                                                                     TINLTCIVKFAPEPPPTVIWSHNREIINFDSPRGGISLVTEKGVLTTSRLLVQKAITQDS
                                                                                                                                                                                                    LTCSTLMLLQLVASC
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                                                                                                                                                                                                                                                                                                                                                                                           VLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWD
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                                                                         Metazoa;
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PubMed=12477932;
Feingold E.A., Grouse
                                                              Chordata;
Primates;
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25,
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EMBL/GenBank/DDBJ
                                                                                                      Last
Last
                                                                                                                           Created)
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                                                                                                                                                                                                                                                                                                                                                                                                               Score 115; DB 5
Pred. No. 0.092;
1; Mismatches 1
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V., Park S., P
                                                              Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                 PRT;
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, Farfan D.,
                                                                                                       sequence up
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  L.H.,
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                                                                                                     on update)
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3J databases.
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Frise E., George
nda A., Mungall C
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Best Local S
Matches 57
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01-MAR-2002
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata
Actinopterygii; Neopterygii;
Ictaluridae; Ictalurus.
    receptor genes.";
proc. Natl. Acad. Sci. U.S.A. 98:13832-13837(2001).
EMBL; AF397467; AAL35555.1; -.
EMBL; AF397455; AAL35543.1; -.
                                                                                                                                                                                                  Hawke N.A., Yoder J.A., Haire R.N., Miracle A.L., Stuge T., Shen L., Mi
                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE=21574523;
                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=7998;
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Proc. Natl. Acad. Sci. U.S.
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                                                                                                                                                         Extraordinary variation in a
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Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Craniata; Vertebrata; Euteleostomi; Teleostei; Ostariophysi; Siluriformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   catfish).
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                                                                                                                                                             R.N., Mueller M.G., Litman R.T., L., Miller N., Litman G.W.; diversified family of immune-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99:16899-16903 (2002).
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Matches
                                                                                                         "Partial sequence of fibulin-6 with a c-terminal region relation in and III of the fibulin family.";

Todomain II and III of the fibulin family.";

Tourist (Apr-2001) to the EMBL/GenBank/DDBJ databases.

REMBL, AJJ06906; CAC37630.1; -.

REGO; GO:0005509; F:calcium ion binding; IEA.

RINterPro; IPR000152; Asx hydroxyl S.

RINterPro; IPR000875; CGCTopin.

RINterPro; IPR000875; CGCTOpin.

RINterPro; IPR006209; EGF Ca.

RINterPro; IPR006209; EGF like.

RINterPro; IPR006209; EGF like.

RINterPro; IPR003598; Ig-Z.

RINTERPro; IPR003598; Ig-Z.

RINTERPRO; IPR003598; Ig-Z.

RINTERPRO; IPR0036984; TSP1.
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InterPro; IPR007110; Ig-like
Pfam; PF0047; Ig; 2.
SMART; SM00409; IG; 2.
PROSITE; PS50835; IG_LIKE;
            Pfam; PF00008; EGF; 5.
Pfam; PF000047; 19; 17.
Pfam; PF00090; TSP1: 6.
PRINTS; PR01705; TSP1: EAT.
SMART; SM00109; EGF CA; 7.
SMART; SM00408; IGCZ; 17.
SMART; SM00209; TSP1; 6.
                                                                                                                                                                                                                                                                                                                                                                                                Q96SC3; PRELIMINARY;
Q96SC3;
01-DEC-2001 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
01-OCT-2003 (TrEMBLrel. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
Eukaryota; Metazoa; (
                                                                                                                                                                                                                                                                                                                                                                          FIBL-6
                                                                                                                                                                                                                                                                                                                                                                                        Fibulin-6
                                                                                                                                                                                                                                                                         Kostka G.,
                                                                                                                                                                                                                                                                                      TISSUE=Melanoma;
                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                       Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO:0004872; F:receptor activity; IEA
                                                                                                   InterPro; IPR008085;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FG----LTANSDTHLLQGQSLTLTLESP-----PGSSPSVQC-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NQGSFLTKGPSKLNDRADSRRSLW-DQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FGEGTELVVQASQHSLS-----VLQQPVHELAHPGGSVTLHCTVITDRCAGEHSVYWFR
                                                                                                                                                                                                                                                                                                                                                                                       (Fragment).
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ASX_HYDROXYL;
                                                                                                                                                                                                                                                                                                                                     Chordata;
Primates;
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; Ig-like.
                                                                                              TSP_1.
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21.7%;
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Last sequence update)
Last annotation update)
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Pred. No. 0.0
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Best Loc
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Matches 66
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PROSITE;
PROSITE;
PROSITE;
PROSITE;
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein DKFZp686H1949.
                                                                                                                                                                                                                                                                                                                                                                        Q7Z3W6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EGF-like
                                                                                                                                                              Fobo G., Han M., Wiemann S.; Submitted (JUN-2003) to the EMBL/GenBank/DDBJ EMBL; BX537377; CAD97619.1; -
                                                                                                                                                                                                 TISSUE=Human amygdala;
Wambutt R., Heubner D., Mewes H.W.,
                                                                                                                                                                                                                                                             Homo варіелв (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae.
                                                                                                                                                                                                                                                                                                                                                Q7Z3W6;
01-OCT-2003
                                                                                                                                          Hypothetical protein. SEQUENCE 338 AA; 3
                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                  DKFZP686H1949
                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                               99
                                                                                              Match rocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        183
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72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; PS00268; CECROPIN; 1.

PS01186; EGF 2; 3.

; PS01187; EGF CA; 8;

; PS50835; IG LIKE; 17.

; PS50092; TSP1; 6.
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                                                                 GVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGIPAPKMTWMKDGRPLPQT--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              domain;
                       N-----QGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVE---- 112
                                                                                                                                                                                                                                                                                                                                                                                                                                  PVITWLRNGERLQATP 704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCLASSPAGDDDKEYLVRVHVPPNIAGTDEPRDITVLRNRQVTLECKSDAVP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LLKAETEDSGKYTCIASNEAGEVSKHFILKVLEPPHINGSEEHEEISVIVNNPLELTCIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -SNQIKILGNQGSFLTKGPSK----LNDRADSRRSLWDQGNFPL------IIK 97
 NDKWSIDPRVIILVNTPTQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PTGSALPDPQTASALP
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                                                                                             Conservative
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                                                                                                                                          37267 MW;
                                                                                                     8.7%;
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20.9%; Pred. No. 1.5
tive 40; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          225
                                                                                           41;
                                                                                           Score 114; DB 4;
Pred. No. 0.11;
1; Mismatches 101
                                                                                                                                         EDD86EE2C57B09E3 CRC64;
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                                             No. 1.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --DQVQTLGGGEVLRISTAQVEDTGRY 635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4;
                                                                                           101;
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YSIMIONVDVYDEGPYTCSVQTDNH
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                                                                                                                                                                                                                                                                           Euteleostomi;
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RESULT 100
Q8N3J6
AC Q8N3J7
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Search completed: A
Job time : 22.7158
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Best Local S
Matches 58
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SMART; SM00409; IG; 2.
SMART; SM00408; IGc; 2.
PROSITE; PS50835; IG_LIKE; 3.
Hypothetical protein; Immunogle
SEQUENCE 435 AA; 47554 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8N3J6;
Q8N3J6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Koehrer K., Beyer A., Mewes H.W., Weil B., Wiemann S.; Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases EMBL; AL834270; CAD38945.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig_c2.
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01-OCT-2003
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58; Conserv
                                                                                                                                                       LPDP---
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                                                                                                                                                                                                                                                                                                      PQEGQPLILTCESKGKPLPEPVLWTKDGGELPDPDRMVVSGRELNILFLNKTDNGTYRCE
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                                                                                                     IRDPNALAGONGPDHALIGGIVAVVVFV
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                                                                                                                                                                                                        ATNTIGQSSAEYVLIVHDVPNTLLPTTIIPSLTTATVTTTVAITTSPTTSA----TTSS
                                                                                                                                                                                                                                                       -TVLQNQKKVEFKI------DIVPRAS----
                                                                                                                                                                                                                                                                                                                                                        --QGQSLTLTLESPPGSSPSVQCRSPRG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                     RSLWDQGNFPLIIKNLKIEDSDTYICEVEDQK----EEVQLLVFGLTANSDTHLL----
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47554 MW; 59DDD4
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Aab67323
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Aar26784
                                                                                                                                                                                                                                                                                              Description
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                                                                                                                                                                    Aar26782
 CD4-kappa
CD4-kappa
CD4-kappa
Human CD4
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Sequence
CD4-gamma
CD4-gamma
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CD4-gamma
Human CD4
CD4-gamma
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CD4-IgG2
CD4-IgG
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CD4-IgG2
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AAR20151
AAR10988
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AAR46679
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AAW02215
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AAP94757
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RESULT 1
AAE37576
ID AAE3
XX AAE3
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XX Huma
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                                            WPI; 2003-441545/41.
N-PSDB; ACC82877.
New CD4 polypeptide ligated at its C-terminus with immunoglobulin, useful for preparing a composition
                                                                                                                                                  25-OCT-2001; 2001US-0346231P
                                                                                                                                                                                 24-OCT-2002; 2002WO-US034393
                                                                                                                                                                                                                                             WO2003040311-A2
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                                                                                                                                                                                                                                                                                                                       219
                                                                                                                                                                                                                                                                         /note= "Wild type Gly substituted with Ala"
                                                                                                                                                                                                                                                                                                                                  /note= "Wild type Glu substituted with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein;
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AAR41043
AAR20148
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AAR07721
AAR04926
AAR04920
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AAP90833
AAP96151
AAP93557
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ABU07697
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a portion of for treating
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Aay14206 HIV -1 Spl

Aay14210 HIV -9120

Aay14210 HIV 99120

Aar15150 pCD4-gels

Aay39824 Soluble h

Aay88327 T4 glycop

Aap93528 Human sol

Aab83356 Human CD4

Aay54500 Amino acoa

Abu07697 Viral coa
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CD4-EBA17
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RESULT 2
AAR26784
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IZ AAR26784
AC AAR2
XX AAR2
XX CD4-CDT 25--P
DT 06-F
CX CD4
XX CD4
XX CD4
XX CD5
XX CD6
XX CD7
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Best Local Similarity
Matches 210; Conserv
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25-MAR-2003
06-FEB-1993
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                                                                                                                                                                                               Domain
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                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
Chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                   homodimer; soluble CD4; T cell receptor; CD4 antigen; high recovery; chimeric; increased serum half life; HIV infection; AIDS; ss.
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                                                        20-AUG-1992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CD4-IgG2 chimeric light chain
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10-FEB-1992;
                                                                                                              WO9213947-A1
                                                                                                                                                                                                                                                              Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPL||KNLKIEDSDTY||CEVEDQKEEVQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PAASAL 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PEVTCV 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TWTCTVLQNQKKVEFKIDIVVLASADKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TWTCTVLQNQKKVEFKIDIVPRASA-----LPAPP-TGSAL----PDPQTASALPDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first
                                                                                                                                                                       1. .205
/label= CD4 domain
206. .310
/label= Ckappa doma
92WO-US001143
                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein; 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entry)
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85.4%;
                                                                                                                                                                       Ckappa domain
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Pred. No. 2.4e.
6; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17;
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120

180 120

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RESULT 3
AAR46680
ID AAR4
AC AAR4
XX AAR4
XX DT 25-M
DT 08-A
XX CD4;
XX CD4;
XX CD4;
XX Human
XX Homo
XX Homo
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence represents a CD4-IgG2 chimeric heavy chain heterotetramer II was produced by expresion of the coding mutagenised cDNA (produced as described in AAQ28089) in Dhfr-CHO cells. The protein is efficiently assembled intracellularly and effectively secreted from mammalian cells pref. CHO, COS, or myeloma cells as a heterotetramer, enabling high recovery and purification from the medium of cells expressing it. It possesses increased serum half-life and has increased avidity for HIV cf. heavy chain dimers. It can inhibit HIV infection of CD4+ cells and block the spread of HIV infection within a patient. Attachment to a detectable marker makes it useful in an assay for HIV or SIV infection, and it can also be linked to toxins, eg Diphtheria, Pseudomonas exotoxin A (domains) I or II) or the deglycosylated A-chain of ricin. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 24-OCT-2003 to standardise OS field)
                                           CD4; gamma; heavy chain; chimeric; chimaeric; immunoconjugate; HIV; human immunodeficiency virus; radionuclide; toxin; therapy; treatme imaging; detection; targetting; immunoglobulin; IgG.
                                                                                                                                             25-MAR-2003
08-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                Homo sapiens
                                                                                                            CD4-kappa light chain.
                                                                                                                                                                                                                           AAR46680 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 16; Fig 5; 90pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CD4-gamma-2 and CD4-IgG2 chimera(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-FEB-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
mes 209; Conserv
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                                                                                                                                                                                                                                                                                                                                      SFLL 244
                                                                                                                                                                                                                                                                                                                                                                                          TWTCTVLQNQKKVEFKIDIVPRASALPAPPTGSALPDPQTASALPDPPAASALPAALAVI
                                                                                                                                                                                                                                                                                                                                                                                                                                     LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               310 AA;
                                                                                                                                                                                                                                                                                                          VCLL
                                                                                                                                                                                                                                                                                                                                                                      TWTCTVLQNQKKVEFKIDIVVLAFTVAAP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78.8%;
ilarity 85.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Maddon
                                                                                                                                           (revised)
(first entry)
                                                                                                                                                                                                                                                                                                          232
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                                                                                                                                                                                                                        protein; 310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1038; DB 2;
Pred. No. 2.8e-64;
4; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and expression vectors -
of HIV infection.
                                                                                                                                                                                                                                                                                                                                                                       -----SVFIFPPSDEQLKSGTASV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 310;
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                                                           therapy; treatment;
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RESULT 4
AAY85081
ID AAY8
XX
AC AAY8
XX
AC 19-J

AAY85081 standard;

protein;

310

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180 180 120 120 60 60

228

AAY85081;

19-JUN-2000

(first entry)

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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                         A tetramer comprising 2 IgG2 heavy chains or two CD4-IgG2 chimeric heavy chains (AAR46679) and two kappa light chains or CD4-kappa light chains is linked to a non-peptidyl toxin or a gamma radiation-emitting radionuclide of low to moderate cytotoxicity. The resulting immunoconjugate comprising the toxin can be used to kill HIV infected cells and to treat HIV infected subjects to reduce the population of HIV infected cells. It can also be used to reduce the likelihood of infection. The immunoconjugate comprising the radionuclide can be used to image HIV infected tissue, to calculate the stage of HIV infection or the efficacy of an anti-HIV treatment using the imaging technique and for determining the prognosis of an HIV infected subject. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Non-peptidyl toxin or radionuclide and CD4-gamma 2 or CD4-IgG2 immuno:conjugates - used to kill HIV-infected cells and to imastage HIV infection.
                                                                                                                                                                                                                                                                                                                                                                 Sequence 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 5; 142pp; English
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229 VCLL 232
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                                                                                                                                                                                                                                                                                                                      Similarity
                            SFLL 244
                                                            TWTCTVLQNQKKVEFKIDIVVLAFTVAAP--
                                                                                    TWTCTVLQNQKKVEFKIDIVPRASALPAPPTGSALPDPQTASALPDPPAASALPAALAVI
                                                                                                                      LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                      LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                    ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                                          MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                     78.8%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ckappa Region
                                                                                                                                                                                                                                                                                                                      Score 1038; DB 2;
Pred. No. 2.8e-64;
                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                        19;
                                                                                                                                                                                                                                                                                                                                      2,
                                                                                                                                                                                                                                                                                                                                   Length 310;
                                                         SVFIFPPSDEQLKSGTASV
                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                        12;
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                                                                                                                                                                                                                                                                                                        Gaps
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CD4-kappa chimeric

light chain amino acid sequence

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This sequence represents the CD4-kappa chimeric light chain amino acid CC sequence of the CD4-IgG2 chimeric heterotetramer. The invention relates to an immunoconjugate comprising a cytotoxic radionuclide and a CC heterotetramer of two heavy chains and two light chains. The cytotoxic radionuclide is linked to either the heavy chains or the light chains, or to all four chains, directly or through a bifunctional chelator. Both CC heavy chains are chimeric CD4-Ig (immunoglobulin) G2 chains encoded by vector CD4-Ig (immunoglobulin) G2 chains encoded by vector CD4-Kappa chains are chimeric CC surface of helper T lymphocytes, cells of the monocyte/macrophage lineage and dendritic cells. CD4 associates with major histocompatibility complex (MMC) class II molecules on the surface of antigen presenting cells to mediate efficient cellular immune response interactions. In humans CD4 is immunoconjugate is used to kill cells infected with HTV, and for treating or preyenting infection, it is also used for imaging HTV-infected tissues (for staging or prognosis of infection, and for assessing efficacy of treatments). The immunoconjugate is also used for determine the HTV envelope glycoprotein burden, once determined, this information is used in the staging and prognosis of HTV infected patients. The constitute assembled intracellularly and secreted efficiently from mammalian calls and cells, allowing high recovery and purification from the culture medium. They have longer half-life in serum and greater avidity than heavy chain call surges and prognosis of inserum and greater avidity than heavy chain call surges and colours and colours.
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06-AUG-1993;
03-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CD4-kappa chimeric light chain; immunoconjugate; treatment; CD4-IgG2; cytotoxic radionuclide; cell surface glycoprotein; prevent; infection; cellular immune response interaction mediator; HIV interaction; staging;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New immunoconjugate, used to treat, prevent or image human immune deficiency virus infection, comprises radionuclide attached to heterotetramer of CD4-immunoglobulin chimeras.
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Allaway GP,
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                                                                                                                                                                                                                                                                                                        Similarity
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ILGNQGSFLTKGPSKLNDRADSRRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                           MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                  MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                                                                                                                                                  Conservative
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93WO-US007422.
95US-00379516.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95US-00477460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; qq82
                                                                                                                                                                                                                                                                                                 78.8%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        English
                                                                                                                                                                                                                                                           Score 1038; DB 3;
Pred. No. 2.8e-64;
4; Mismatches 19
                                                                                                                                                                                                                                                                                                                                       DB 3;
                                                                                                                                                                                                                                                                  19;
                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                       310;
                                                                                                                                                                                                                                                              12;
                                                                                                                  60
                                                                                                                                                                                      60
                                             120
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13

ILGNQGSFLTKGPSKLNDRADSRRSLMDQGNFFLIIKNLKIEDSDTYICEVEDQKEEVQL

MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKS1QFHWKNSNQIK

MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK

60 60

120

209;

Conservative

4.

Indels

12;

Gaps

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RESULT 5
AAB67324
ID AAB6
XX AAB6
XX AAB6
XX AAB6
XX Inmu
PF 03-1
PR 07-1
PR 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ś
  Best Loc
Matches
                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                   comprising kappalight
                                                                                                                                                                                                                The present invention relates to an immunoconjugate, comprising a cytotoxic radiomuclide linked, directly or via a bifunctional chelator, to a heterotetramer having two chimeric CD4-IGG2 heavy chains encoded by an expression vector CD4-IGG2HC-pRcCMV and two chimeric CD4-kappa light chains encoded by an expression vector CD4-IGG2HC-pRcCMV. The invention is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-FEB-1995;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-AUG-1992;
06-AUG-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB67324 standard;
                                                                                                              Sequence 310
                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-158582/16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Maddon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US6177549-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CD4-kappa chimeric light chain protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB67324;
                                                                                                                                                                                                  useful for killing human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunoconjugate for treating human immunodeficiency virus-infected subject, consists of cytotoxic radionuclide linked to heterotetram comprising two chimeric CD4-IgG2 heavy chains and two chimeric CD4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunoconjugate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (PROG-) PROGENICS PHARM INC
                                                                                                                                                                        treatment and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               229 VCLL 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PJ,
                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SFLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TWICTVLQNQKKVEFKIDIVVLAFTVAAP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TWTCTVLQNQKKVEFKIDIVPRASALPAPPTGSALPDPQTASALPDPPAASALPAALAVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Allaway
                                                                                                                 ₽
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92US-00927931.
93WO-US007422.
95US-00379516.
95US-00477460.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9908-00329916.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chelator; chimeric; HIV; human
                                                                                                                                                                     prevention
                                                                                                                                                                                                                                                                                                                                                                                               43pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein; 310 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entry.
                             78.8%;
                                                                                                                                                               immunodeficiency virus (HIV) -infected cells, tion of infection with HIV
Score 1038; DB 4;
Pred. No. 2.8e-64;
4; Mismatches 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----SVFIFPPSDEQLKSGTASV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             inked to heterotetramer and two chimeric CD4-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immunodeficiency virus
                                                    Length 310;
                                                                                                                                                                                                  for
                                                                                                                                                                                                                                                                                γď
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RESULT 6
AAB80885
ID AAB8
XX Huma
XX Huma
XX Huma
XX Homc
XX Inhe
PR 08-F
PR 0
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Query Match
Best Local Similarity 85.7
Matches 209; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-FEB-1991;
10-FEB-1992;
08-DEC-1992;
                                                                                                                                                           The present invention relates to a method for inhibiting infection of a CD4+ cell by HIV. The method comprises contacting the HIV with a CD4-IgG2 chimexic heterotetramer to form a complex with the HIV (CD4 = cluster of differentiation 4; IgG2 = immunoglobulin gamma 2). CD4 is a cell surface glycoprotein that is expressed primarily on the surface of T cells. In man, CD4 is the target of interaction with HIV. The heterotetramer has two heavy and two light chains which are encoded by expression vectors CD4-IgG2CHC-pRcCMV (V1) and CD4-kLC-pRcCMV (V2), respectively. The method is used to inhibit infection of a CD4+ cell by a HIV and to prevent CD4+cells of a subject from becoming infected with HIV. The method is also useful for treating a subject having CD4-cells infected with HIV. The present sequence is human fusion protein: CD4-kappa chimeric light chain of the CD4-IgG2 chimeric heterotetramer. This sequence was used in the method of the present invention
                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-264981/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US6187748-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; Anti-HIV; CD4
immunoglobulin gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human CD4-kappa chimeric light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB80885 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (PROG-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nibiting human immunodeficiency virus (HIV) infection of a CD4+ or treating a subject having CD4+ cells infected with HIV involves 4-IgG2 chimeric heterotetramer to form a complex with the HIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROGENICS PHARM
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                                                                                                               310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fig 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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92WO-US001143.
92US-00960440.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9505-00485372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CD4-IgG2 chimeric heterotetramer; amma 2; CD4-kappa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein; 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GA;
                          78.8%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INC
Score 1038; DB 4;
Pred. No. 2.8e-64;
4; Mismatches 19;
                                                 Length 310;
  Indels
  12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  240
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                                                                                                                                                                                          Novel CD4-immunoglobulin G2 chimeric heterotetramer neutralizes human immunodeficiency virus-1 with two heavy and light chains encoded by expression vectors designated CD4-IgG2HC-pRcCMV and CD4-kLC-pRcCMV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-FEB-1992;
08-DEC-1992;
                                                                                                                         Claim
                                                                                                                                                                                                                                                                                                 WPI; 2003-038273/03.
N-PSDB; ABS55722.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-FEB-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                           (PROG-)
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                                                                                                                    1; Fig
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                                                                                                                       5A-D;
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92WO-US001143.
92US-00960440.
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/label=_Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Mature CD4-kappa chimeric light chain of the CD4-
IgG2 chimeric heterotetramer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26. .310
                                                                                                                    54pp;
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                                                                                                                    English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of the CD4-IgG2 chimeric protein.
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heterotetramer (I) t 1) having two heavy -IgG2HC-pRcCMV, and

The invention describes a purified CD4-immunoglobulin (Ig)G2 chimeric heterotetramer (I) that neutralises human immunodeficiency virus-1 (H.

chains encoded by an expression vector two light chains encoded by expression

designated vector

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RESULT 8
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Best Local S
Matches 209
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                                                                                                                                                                                                 New CD4 polypeptide ligated at its C-terminus with immunoglobulin, useful for preparing a composition preventing HIV-1 infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; CD4; cluster of differentiation factor 4; immunoglobulin; Ig; human immunodeficiency virus; gene therapy; vaccine; HIV-1 infection; D2; alpha tailpiece; alphatp; fusion protein.
The invention relates to a polypeptide ligated at its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human D1D2-Ig alphatp fusion
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                                                                                                                     Example 1; Page 47; 100pp; English
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DB; AAD29113.
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Matches 208
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28-JAN-1993
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428. .534
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25-MAR-2003
06-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human gamma 1 heavy chain gene, the plasmid pBr gamma 1 is digested with SacII, and the SacII sites are then made flush using T4 DNA polymerase. The fragment containing the CH1 exon is then purified and ligated to the M13mpl8(CD4) vector. Oligonucleotide-mediated site-directed mutagenesis is then performed to juxtapose the CD4 and CH1 sequences in frame. The CD4-CH1 chimeric gene is then linearized and ligated to the Pst1-Pst1 DNA fragment of the plasmid pBr gamma 1 containing the hinge, CH2, and CH3 exons of the human gamma 1 chain gene designated CD4-1gG1HC-pRcCMV (ATCC 75192). (Updated on 25-MAR-2003 to correct PN field.)
                                                       Domain
                                                                                                                                                          Chimeric
                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                  homodimer;
chimeric;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CD4-gamma 1 chimeric heavy chain homo-dimer and its expression vector - for preventing and treating HIV infection useful as a diagnostic agent.
             WO9213947-A1
                                                                                  Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TWTCTVLQNQKKVEFKIDIVVLAFASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TWTCTVLQNQKKVEFKIDIVPRA------SALPAPPT-----GSA------LPDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  534 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fig 4; 88pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                                                                                 ; soluble CD4; T cell receptor; CD4 antigen; high recovery; increased serum half life; HIV infection; AIDS; ss.
                                                                                                                                                                                                                                            chimeric heavy chain homodimer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                        (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                222
                                                                                                                                                                                                                                                                                                     revised)
                                        217. .325
/label= CH2
326. .433
/label= CH3
                                                                                                                            Location/Qualifiers
                                                                                                 label=
                                                                                                                                                                                                                                                                                                                                                         protein; 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78.4%;
85.7%;
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                                                                                                  CD4
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Pred. No. 1.2e-63;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22;
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RESULT 11
AAR46678
ID AAR46
XX CD4-9
XX CD4,
XX CD4,
XX Imagi
XX Imagi
XX Homo
XX Homo
XX Homo
XX Homo

CD4-gamma 2

chimeric heavy chain.

CD4; gamma; heavy chain; chimeric;

human immunodeficiency virus; radionuclide; toxin; therapy; treatment;

chimaeric; immunoconjugate; HIV;

imaging; detection; targetting.

Homo sapiens

Location/Qualifiers

25-MAR-2003 08-AUG-1994

(revised) (first en

entry)

AAR46678; AAR46678

standard; protein;

432

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180

180

120 120 60 60

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                     This sequence represents a CD4-gamma2 chimeric heavy chain homodimer. It was produced by expresion of the coding mutagenised cNNA (produced as described in AAQ28088) in Dhfr-CHO cells. The protein is efficiently assembled intracellularly and effectively secreted from mammalian cells pref. CHO, COS, or myeloma cells as a homodimer, enabling high recovery and purification from the medium of cells expressing it. It possesses increased serum half-life and has increased avidity for HIV of. heavy chain dimers. It can inhibit HIV infection of CD4+ cells and block the spread of HIV infection within a patient. Attachment to a detectable marker makes it useful in an assay for HIV or SIV infection, and it can also be linked to toxins, eg Diphtheria, Pseudomonas exotoxin A (domains) I or II) or the deglycosylated A-chain of ricin. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 24-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CD4-gamma-2 and CD4-IgG2 chimera(s) treatment, prevention and diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1992-300034/36.
N-PSDB; AAQ28088.
                                                                                                                                                                                                                                                                                                                                          Sequence 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 2; Fig 3; 90pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Beaudry GA,
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                                                                                                                                                                                                                                                                                     Local
181
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                                                                                                                                                                                                                           1 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
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                                                                                                                                                                                                                                                                                         Similarity
                     TWTCTVLQNQKKVEFKIDIV----PRASALPAPPTGSALPDPQTASALPDPPAA 230
                                                                 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                          LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                    ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                MRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
TWTCTVLQNQKKVEFKIDIVVLAFERKCCVECPP---
                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                          AA;
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                                                                                                                                                                                                                                                                                       78.4%;
                                                                                                                                                                                                                                                                         1;
                                                                                                                                                                                                                                                                                         Score 1032.5;
Pred. No. 9.96
                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and expression vectors of HIV infection.
                                                                                                                                                                                                                                                                                                        DB 2;
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 ----CPAPPVA
                                                                                                                                                                                                                                                                                                        432;
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 221
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RESULT 12
AAY85079
ID AAY85
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AC AAY85
XX
AC AAY85
XX
DT 19-JU
XX
DE Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                             A CD4-gamma 2 chimeric heavy chain homodimer is linked to a non- peptidyl toxin or a gamma radiation-emitting radionuclide of low to moderate cytotoxicity. The resulting immunoconjugate comprising the toxin can be used to kill HIV infected cells and to treat HIV infected subjects to reduce the population of HIV infected cells. It can also be used to reduce the likelihood of infection. The immunoconjugate comprising the radionuclide can be used to image HIV infected tissue, to calculate the stage of HIV infection or the efficacy of an anti-HIV treatment using the imaging trechnique and for determining the prognosis of an HIV infected subject. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Non-peptidyl toxin or radionuclide and CD4-gamma 2 or CD4-IgG2 immuno:conjugates - used to kill HIV-infected cells and to ima
 Human CD4-gamma 2 chimeric heavy chain homodimer amino acid sequence
                             19-JUN-2000
                                                                                  AAY85079 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 3; 142pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              stage HIV infection.
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206; Conserv
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                                                                                                                                                                                                                            LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                         TWTCTVLQNQKKVEFKIDIV----PRASALPAPPTGSALPDPQTASALPDPPAA 230
                                                                                                                                                                                                                                                                  ILGNOGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                                                                                     | ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                                                                                                                                         MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                                                                                                                                                                                                                                                                                                                      432 AA;
                                                                                                                                                      TWTCTVLQNQKKVEFKIDIVVLAFERKCCVECPP-------CPAPPVA 221
                                                                                                                                                                                                            LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                                                                                                                                                         MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
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                           (first entry)
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/label=
21
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                                                                                  protein; 432
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88.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CD4 Region.
                                                                                                                                                                                                                                                                                                                                                                             Score 1032.5; DB:
Pred. No. 9.9e-64;
1; Mismatches 10
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                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                          432;
                                                                                                                                                                                                                                                                                                                                                                               17;
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CD4-gamma 2 chimeric heavy chain homodimer; immunoconjugate; treatment; cytotoxic radionuclide; cell surface glycoprotein; prevent; infection; cellular immune response interaction mediator; HIV interaction; staging prognosis; envelope glycoprotein burden; human.
                                                                                                                                                                          06-AUG-1993;
03-FEB-1995;
N-PSDB; AAZ98855.
                                                                          Allaway GP, Maddon
                                                                                                                                                                                                                             07-AUG-1992;
                                                                                                                                                                                                                                                                                  07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                        US6034223-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                             (PROG-) PROGENICS PHARM INC
                        2000-269502/23.
                                                                                                                                                                                                     92US-00927931.
93WO-US007422.
                                                                                                                                                                             95US-00379516.
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New immunoconjugate, used to treat, prevent or image human immune deficiency virus infection, comprises radionuclide attached to heterotetramer of CD4-immunoglobulin chimeras.

Disclosure; Fig 3; 58pp; English.

This sequence represents the human CD4-gamma 2 chimeric heavy chain CC immunoconjugate comprising a cytotoxic radionuclide and a heterotetramer of two heavy chains and two light chains. The cytotoxic radionuclide is CC chains, directly or through a bifunctional chelator. Both heavy chains and two light chains. The cytotoxic radionuclide is CC chains, directly or through a bifunctional chelator. Both heavy chains CC chains, or to all four CC chains, directly or through a bifunctional chelator. Both heavy chains CC chains encoded by vector CD4-TG (immunoglobulin) G2 chains encoded by vector CD4-TG (immunoglobulin) G2 chains are chimeric CD4-kappa CC chains encoded by vector CD4-TG (immunoglobulin) G2 chains are chimeric CD4-kappa CC chains encoded by vector CD4-Kappa CC (hains encoded by vector CD4-Kappa CC (hains encoded by vector CD4-Kappa CC (chains encoded by vector CD4-Kappa CC (hains encoded by vector CD4-Kappa CC (mains encoded by vector CD4-Kappa CC (hains encoded by vector CD4-Kappa CC (hains encoded by vector CD4-Kappa CC (hains encoded by vector CD4-Kappa CC (mains encoded by vector CD4-Kappa CC (hains encoded by vector CD4-Kappa CC (mains encoded by vector CD4-Kappa CC (mains encoded by vector CD4-Kappa CD4 is the stage of collular immune response interactions In humans CD4 is the target of interaction with the human immunodeficiency virus HIV. The communoconjugate is used to kill cells infected with HIV, and for treating CC (for staging or prognosis of infection, and for assessing efficacy of CC (reatments). The immunoconjugate is also used for imaging HIV-infected tissues CC (for staging and prognosis of HIV infected patients. The used in the staging and prognosis of HIV infected patients. The communoconjugate should be active against all strains of HIV (since the CC 44-gpl20 interaction is essential for infection). The heterotetramers CC are assembled intracellularly and secreted efficiently than heavy chain CC dimens of the coll of the co

Sequence 432 \$

Similarity

78.4%;

.9e-64; DB 3;

Length 432;

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Best Local S
Matches 206
                                                                                                        206;
13
                        61
                                                               MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                 MNRGVPFRHLLLVLQLALLPAATQSKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                      Conservative
                                                                                                     Score 1032.5;
Pred. No. 9.9e-
1; Mismatches
                                                                                                      10;
                                                                                                      Indels
                                                                                                        17;
                                                                                                        Gaps
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ARESULT 13
AAB67322
ID CD4-9
IC CD4-9
IMMUI
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IMMU
PR 07-AI
CC CThe I
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CC Cytol
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                       Matches 206;
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06-AUG-1993;
03-FEB-1995;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to an immunoconjugate, comprising a cytotoxic radionuclide linked, directly or via a bifunctional chelator, to a heterotetramer having two chimeric CD4-IGG2 heavy chains encoded by an expression vector CD4-IGG2HC-pRcCMV and two chimeric CD4-kappa light chains encoded by an expression vector CD4-KLC-pRcMV. The invention is useful for killing human immunodeficiency virus (HIV)-infected cells, for the treatment and prevention of infection with HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       subject, consists of cyt comprising two chimeric kappalight chains.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunoconjugate for treating human immunodeficiency virus-infected subject, consists of cytotoxic radionuclide linked to heterotetramer comprising two chimeric CD4-IgG2 heavy chains and two chimeric CD4-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunoconjugate;
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121
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                         LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180
                                                                                                                                                                                                                                              MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                                                                                                                                                                                                                                  432 AA;
                                                                                                                                                                                                             MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
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                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fig 3; 43pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Allaway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry
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93WO-US007422.
95US-00379516.
95US-00477460.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chelator; chimeric; HIV; human immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein;
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မှ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       heavy
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88.0%;
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                                                                                                                                                                                                                                                                                                                  Score 1032.5; DB
Pred. No. 9.9e-64;
1; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ₹
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                                                                                                                                                                                                                                                                                                                       Indels
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ILGNQGSFLTKGPSKLNDRADSRRSLMDQGNFFLIIKNLKIEDSDTYICEVEDQKEEVQL
ILGNQGSFLTKGPSKLNDRADSRRSLMDQGNFFLIIKNLKIEDSDTYICEVEDQKEEVQL
ILGNQGSFLTKGPSKLNDRADSRRSLMDQGNFFLIIKNLKIEDSDTYICEVEDQKEEVQL
LVFGLTANSDTHLLQGQSLTLTLESPFGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG

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                                                             Query Match
Best Local Similarity
Matches 206; Conser
                                                                                                                                                     The present invention relates to a method for inhibiting infection of a CD4+ cell by HIV. The method comprises contacting the HIV with a CD4-IgG2 chimeric heterotetramer to form a complex with the HIV (CD4 = cluster of differentiation 4; IgG2 = immunoglobulin gamma 2). CD4 is a cell surface glycoprotein that is expressed primarily on the surface of T cells. In man, CD4 is the target of interaction with HIV. The heterotetramer has two heavy and two light chains which are encoded by expression vectors CD4-IgC2HC-pRcCMV (VI) and CD4-kIC-pRcCMV (V2), respectively. The method is used to inhibit infection of a CD4+ cell by a HIV and to prevent CD4+cells of a subject from becoming infected with HIV. The method is also useful for treating a subject having CD4+ cells infected with HIV. The present sequence is human fusion protein: CD4-gamma2 chimeric heavy chain homodimer. This sequence was used in the method of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                   Inhibiting human immunodeficiency virus (HIV) infection of a CD4+ cell, or treating a subject having CD4+ cells infected with HIV involves using CD4-IgG2 chimeric heterotetramer to form a complex with the HIV.
                                                                                                                            Sequence 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-FEB-1992;
08-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-FEB-1991;
                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 3; 55pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-FEB-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; Anti-HIV; CD4-IgG2 chimeric heterotetramer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human CD4-gamma2 chimeric heavy chain homodimer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (PROG-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunoglobulin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROGENICS PHARM INC
MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                             MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
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                                                                Conservative
                                                                                                                            A,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91US-00653684.
92WO-US001143.
92US-00960440.
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                                                                              78.4%;
88.0%;
                                                                                                                                                                                                                                                                                                                                                                                   English
                                                             1;
                                                                            Score 1032.5; DB 4;
Pred. No. 9.9e-64;
                                                                Mismatches
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                                                             Indels
                                                                                           Length
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                                                                              Query Match
Best Local S
Matches 206
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10-FEB-1992;
08-DEC-1992;
                                                                                                                                                                                                                           The invention describes a purified CD4-immunoglobulin (Ig)G2 chimeric heterotetramer (I) that neutralises human immunodeficiency virus-1 (HIV-1) having two heavy chains encoded by an expression vector designated CD4-IgG2HC-pRCCMV, and two light chains encoded by expression vector designated CD4-kLC-pRCCMV. (I) and a composition (II) comprising (I) or (I) linked to a toxin, are useful for inhibiting HIV infection of a CD4 cell, and preventing a subject being infected with HIV by blocking the spread of HIV infection. This is the amino acid sequence of the CD4-gamma2 chimeric heavy chain of the CD4-IgG2 chimeric heterotetramer useful in inhibiting HIV infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel CD4-immunoglobulin G2 chimeric heterotetramer neutralizes human immunodeficiency virus-1 with two heavy and light chains encoded by expression vectors designated CD4-IgG2HC-pRcCMV and CD4-kLC-pRcCMV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CD4; gamma2 mutein.
                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide
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                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABS55720.
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MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TWTCTVLQNQKKVEFKIDIV----PRASALPAPPTGSALPDPQTASALPDPPAA 230
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                                                                                Conservative
                                                                                                                                                                              ₽,
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92WO-US001143.
92US-00960440.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3A-F; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note=
-IgG2 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= Signal_peptide
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                                                                                                     78.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   = "Mature chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human immunodeficiency virus-1;
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                                                                         Score 1032.5; DB 6;
Pred. No. 9.9e-64;
1: Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CD4-gamma2 chimeric heavy heterotetramer"
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                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-OCT-2003
25-MAR-2003
06-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                               homodimer;
chimeric;
                                     This sequence represents a CD4-IgG2 chimeric heavy chain heterotetramer It was produced by expresion of the coding mutagenised cDNA (produced as described in AAQ28089) in Dhfr-CHO cells. The protein is efficiently assembled intracellularly and effectively secreted from mammalian cells
                                                                                                                                                                                                                                                                                                                        Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CD4-IgG2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR26783;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR26783
                                                                                                                     CD4-gamma-2 and CD4-IgG2 chimera(s)
                                                                                                                                                                                                              08-FEB-1991;
                                                                                                                                                                                                                                                                                                      Domain
                                                                                                                                                                                                                                                                                                                                             Domain
                                                                                                                                                                                                                                                                                                                                                                 Domain
                                                                                                                                                                                                                                                                                                                                                                                               Key
                                                                                                                                                                                                                                                                                                                                                                                                                   Chimeric
                                                                                        Claim
                                                                                                           treatment,
                                                                                                                                                                      Beaudry GA, Maddon
                                                                                                                                                                                                                                  10-FEB-1992;
                                                                                                                                                                                                                                                      20-AUG-1992.
                                                                                                                                                                                                                                                                         WO9213947-A1.
                                                                                                                                                                                                                                                                                                                                                                                     Domain
                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                          (PROG-)
                                                                                                                                        1992-300034/36.
DB; AAQ28089.
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                                                                                                                                                                                          PROGENICS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chimeric heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFFLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TWICTVLQNQKKVEFKIDIVVLAFERKCCVECPP-----CPAPPVA 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TWTCTVLQNQKKVEFKIDIV----PRASALPAPPTGSALPDPQTASALPDPPAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ILGNOGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                       Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                               ; soluble CD4; T cell receptor; increased serum half life; HIV
                                                                                                          prevention and diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (revised)
(first entry)
                                                                                       4; 90pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (revised)
                                                                                                                                                                                                              91US-00653684.
                                                                                                                                                                                                                                  92WO-US001143
                                                                                                                                                                                                                                                                                                                                   /label=
                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                             'label= CH3 domain
                                                                                                                                                                                                                                                                                                                                                       'label=
                                                                                                                                                                                                                                                                                                                                                                          label= CD4 domain
                                                                                                                                                                                                                                                                                                                abel=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein;
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                                                                                                                                                                                                                                                                                                                                             .312
                                                                                       English.
                                                                                                                                                                                                                                                                                                                 CH2
                                                                                                                                                                                                                                                                                                                                  hinge domain
                                                                                                                                                                                                                                                                                                                                                       CH1 domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            530
                                                                                                                                                                                                                                                                                                                domain
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                                                                                                           and expression vectors of HIV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                               CD4 antigen; high infection; AIDS; s
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pref. CHO, COS, or myeloma cells as a heterotetramer, enabling high recovery and purification from the medium of cells expressing it. It possesses increased serum half-life and has increased avidity for HIV cf. heavy chain dimers. It can inhibit HIV infection of CD4+ cells and block

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RESULT 17
AAY85080
ID AAY85
XX AAY85
XX 19-JU
XX CD4-I
XX CD4-I
XX CD4-I
XX CD4-I
XX CD4-I
XX CD4-I
XX CO1-I
XX CO1-I
XX CO1-JI
XX O7-AI
PR 03-FI
XX X IPRO
XX IPRO
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                            07-AUG-1992;
06-AUG-1993;
03-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CD4-IgG2 chimeric heavy chain heterotetramer; immunoconjugate; treatment; cytotoxic radionuclide; cell surface glycoprotein; prevent; infection; cellular immune response interaction mediator; HIV interaction; staging;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the spread of HIV infection within a patient. Attachment to a detectable marker makes it useful in an assay for HIV or SIV infection, and it can also be linked to toxins, eg Diphtheria, Pseudomonas exotoxin A (domains I or II) or the deglycosylated A-chain of ricin. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 24-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        prognosis; envelope glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CD4-IgG2 chimeric heterotetramer heavy chain amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-JUN-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY85080 standard; protein; 530 AA
                             Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                               New immunoconjugate, used to treat, prevent or image human immune deficiency virus infection, comprises radionuclide attached to heterotetramer of CD4-immunoglobulin chimeras.
                                                                                                                                                                                                 2000-269502/23.
DB; AAZ98856.
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                                                                                                                                                                                                                                                                                                                                           PROGENICS PHARM INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SFLL 244
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                          Fig 4; 58pp; English
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                                                                                                                                                                                                                                                                                   Maddon PJ
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93WO-US007422.
95US-00379516.
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84.8%;
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23-JAN-2001

Immunoconjugate; chelator; chimeric; HIV; human immunodeficiency virus.

CD4-IgG2 chimeric heavy chain protein.

23-APR-2001

(first entry)

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RESULT 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CC This sequence represents the CD4-IgG2 chimeric heavy chain amino acid companies from the CD4-IgG2 chimeric heterotetramer. The invention relates communication and immunoconjugate comprising a cycotoxic radionuclide and a companies of two heavy chains and two light chains. The cytotoxic radionuclide is linked to either the heavy chains or the light chains, or companies are chimeric CD4-Ig (immunoglobulin) G2 chains encoded by vector CD4-Ig(immunoglobulin) G2 chains are chimeric CD4-Ig (immunoglobulin) G2 chains encoded by vector CD4-Kappa chains encoded by vector CD4-Ig-PRCMV (ATCC 75193) and both light chains are chimeric CC CD4-kappa chains encoded by vector CD4-Kappa chains encoded by vector CD4-Kappa chains encoded by vector CD4-Ig-PRCMV (ATCC 75194). CD4 is a compolymorphic cell surface glycoprotein that is expressed on the compolymorphic cells. CD4 associates with major histocompatibility complex (MHC) class II molecules on the surface of antigen presenting cells to mediate efficient cellular immunor response interactions. In humans CD4 is the target of interaction with the human immunodeficiency virus HIV. The immunoconjugate is used to kill cells infected with HIV, and for treating cor preventing infection, infection, and for assessing efficacy of cor preventing infection. It is also used for imaging HIV-infected tissues (for staging or prognosis of infection, and for assessing efficacy of communoconjugate is also used to determine the HIV envelope glycoprotein burden, once determined, this information is used in the staging and prognosis of HIV infected patients. The immunoconjugate should be active against all strains of HIV (since the CD4 are assembled intracellularly and secreted efficiently from mammalian cells, allowing high recovery and purification from the culture medium. They have longer half-life in serum and greater avidity than heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 207
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                                                                                                                                                                                                                                                                                                             AAB67323 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                241
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06-AUG-1993;
03-FEB-1995;
07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunoconjugate for treating human immunodeficiency virus-infected subject, consists of cytotoxic radionuclide linked to heterotetramer comprising two chimeric CD4-IgG2 heavy chains and two chimeric CD4-kappalight chains.
                                                      US6187748-B1
                                                                                                                                                             immunoglobulin
                                                                                                                                                                                                                                              Human CD4-IgG2 chimeric heavy chain.
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                                                                                                                                                                                          Anti-HIV; CD4-IgG2
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93WO-US007422.
95US-00379516.
95US-00477460.
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84.8%;
                                                                                                                                                                                             chimeric heterotetramer;
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Matches 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chimeric heterotetramer to form a complex with the HIV (CD4 = cluster of differentiation 4; IGG2 = immunoglobulin gamma 2). CD4 is a cell surface glycoprotein that is expressed primarily on the surface of T cells. In man, CD4 is the target of interaction with HIV. The heterotetramer has two heavy and two light chains which are encoded by expression vectors CD4-IGG2HC-pRcCMV (VI) and CD4-kLC-pRcCMV (V2), respectively. The method is used to inhibit infection of a CD4+ cell by a HIV and to prevent CD4+ cells of a subject from becoming infected with HIV. The method is also useful for treating a subject having CD4+ cells infected with HIV. The prevent consecutively is human fusion protein: CD4-Ig2 chimeric heavy chain of the CD4-Ig32 chimeric heavy chain of the CD4-Ig32 chimeric heavy chain of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to a method for inhibiting infection of a CD4+ cell by HIV. The method comprises contacting the HIV with a CD4-IgG2 chimeric heterotetramer to form a complex with the HIV (CD4 = cluster of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Inhibiting human immunodeficiency virus (HIV) infection of a CD4+ cell, or treating a subject having CD4+ cells infected with HIV involves using CD4-IgG2 chimeric heterotetramer to form a complex with the HIV.
                                                                                                                                        ABG71123 standard;
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                                                                    17-JAN-2003
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                                                                                                                                                                                                                                                                 SFLL 244
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92WO-US001143.
92US-00960440.
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CD4-immunoglobulin

G2 (IgG2)

chimeric heterotetramer.

immunoglobulin

G2 ;

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gamma2; human

immunodeficiency virus-1; HIV-1;

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10-FEB-1992;
08-DEC-1992;
                                                                                                                                                                                                                                                                                                                                              The invention describes a purified CD4-immunoglobulin (Ig)G2 chimeric heterotetramer (I) that neutralises human immunodeficiency virus-1 (HIV-1) having two heavy chains encoded by an expression vector designated CD4-IgG2HC-pRcCMV, and two light chains encoded by expression vector designated CD4-kLC-pRcCMV. (I) and a composition (II) comprising (I) or (I) linked to a toxin, are useful for inhibiting HIV infection of a CD4-cell, and preventing a subject being infected with HIV by blocking the spread of HIV infection. This is the amino acid sequence of the CD4-immunoglobulin G2 chimeric heavy chain chimeric heterotetramer useful in inhibiting HIV infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel CD4-immunoglobulin G2 chimeric heterotetramer neutralizes human immunodeficiency virus-1 with two heavy and light chains encoded by expression vectors designated CD4-IgG2HC-pRcCMV and CD4-kLC-pRcCMV,
                                                                                                                                                                                                                                                                                                                         Sequence
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GCLV 233
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                                                                                                      LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                           ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                 TWTCTVLQNQKKVEFKIDIVPRASALPAPPTGSALPDPQTASALPDPPAASALPAALAVI
                                                                                                                                                                            ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                               MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                                                                                                                                                                                                        530 AA;
                                                   TWTCTVLQNQKKVEFKIDIVVLAFASTKGP---
                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91US-00653684.
92WO-US001143.
92US-00960440.
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/label=_Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                               78.2%;
84.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Mature CD4-IgG2 chimeric heterotetramer"
                                                                                                                                                                                                                                                                    5
                                                                                                                                                                                                                                                                 Score 1030.5; DB 6;
Pred. No. 1.7e-63;
5; Mismatches 21;
                                                   SVFPLAPCSRSTSESTAAL
                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                             530;
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                                                                                                                                                                                                                                                                   Gaps
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RESULT 21
RAR78674
ID AAR78674
XX AAR78
XX AAR78
XX CD4 c
XX Chime
KW human
XX Homo
XX
AAR89451
ID AARI
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AC AARI
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DT 26-4
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                                                                                                                                           RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 200; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Extracellular domains D1-D4 (AAR78673) or D1-D2 (AAR78674) of human CI are used in the construction of chimeric receptors utilised in the targeted cytolysis of cells expressing HIV envelope proteins on their surface. The chimeric receptors comprise the extracellular domain (pre amino acids 1-394 or 1-200) of CD4 linked to an intracellular portion,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Target
cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1995-292893/38
N-PSDB; AAQ96104.
                                                                                           AAR89451 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-FEB-1994;
02-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chimeric receptor; CD4; human immunodeficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 10; Fig 24; 118pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-JAN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9521528-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GEHO)
                                                                                                                                                                                                                181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cytolysis of HIV-infected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T-cell receptor protein zeta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GEN HOSPITAL
                                                                                                                                                                                                                                            TWTCTVLQNQKKVEFKIDIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 203
                                                                                                                                                                                                              TWTCTVLQNQKKVEFKIDIV
                                                                                                                                                                                                                                                                                                            LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                                                                                                                                                                        LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                                                                                                                                                                                                                                      ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                                                                                                                                                                                                                               ILGNQGSFLTKGPSKLNDRADSRRSLMDQGNFFLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKS1QFHWKNSNQIK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78.1%; S ilarity 100.0%; Conservative 0;
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94US-00284391
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                                                                                           peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CD4; T-cell receptor;
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                                                                                              203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1029; DB 2;
Pred. No. 7.5e-64;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunotherapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytolysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       intracellular domain (pref.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 203;
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26-SEP-1996 AAR89451;

(first entry)

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Best Local S
                                                                                                                                                                                                                                                                                                                                               This sequence represents the CD4 D1-D2 domains of CD4. This sequence is included in the membrane bound proteinaceous chimeric receptor of the invention. The extracellular portion of the chimeric receptor contains a fragment of CD4 (amino acids 1-394 or 1-200 of the CD4 sequence) which specifically recognises and binds HIV-infected cells, but does not mediate HIV infection. The extracellular domain of the receptor is separated from the cell membrane by 48 or 72 angstroms, or by one or more proteinaceous alpha-helices. The transmembrane region of the chimeric receptor contains a portion of the CD7. CD5 or CD34 transmembrane domain. Alternatively, the extracellular portion of the receptor can also be separated from the intracellular domain by the hinge, CH2 and CH3 domains of human IgG1. The cells expressing the receptor are preferably T cells, neutrophils, or dendritic cells. The therapeutic cells expressing the chimeric receptor are administered to a mammal to treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Membrane-bound chimeric receptor comprising extracellular including CD4 fragment - cells expressing receptor can be treatment of HIV infection.
                                                                                                                                                                                                                                                                                                                                      expressing the chimeric HIV infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-AUG-1994;
24-FEB-1995;
                                                                                                                                                                                                                                                                                                         Sequence 203 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 10; Fig 24; 134pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          dendritic cell; therapy; mammal; infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CD7; transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CD4 D1-D2 domains.
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                            181
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181
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                                                                                                                                                                                                                                               200;
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                                                                                                                                                                                                                                                              Similarity
                   TWTCTVLQNQKKVEFKIDIV 200
                                                                                                                                                                               MIRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                                                                                   MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKS1QFHWKNSNQIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Banapour B,
                                                                               LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
 TWTCTVLQNQKKVEFKIDIV 200
                                                           LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                      ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                            ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                                               Conservative
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95US-00394388.
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                                                                                                                                                                                                                                       78.1%; Suc.
100.0%; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Romeo
                                                                                                                                                                                                                                            Score 1029; DB 2;
; Pred. No. 7.5e-64;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G
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                                                                                                                                                                                                                                                                         Length 203;
                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  portion portion
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                                                                                                                                                                                                                                               Gaps
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RESULT 23
AAR78673
ID AAR78

AAR78673

standard;

protein; 398

CD4 D1-D4 domains 26-SEP-1996 AAR89450

(first

AAR89450 standard;

peptide;

398

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RESULT 24
AAR89450
ID AAR85
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AC AAR89
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DT 26-SE
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DE CD4 [
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Best Local S
Matches 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chimeric receptor; CD4; T-cell receptor; HIV; cytolysis; human immunodeficiency virus; adoptive immunotherapy.
                                                                                                                                                                                                                                                                                                                                                                       Sequence 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Target cytolysis of HIV-infected cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1995-292893/38.
N-PSDB; AAQ96103.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-FEB-1994;
02-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 10; Fig 23; 118pp; English.
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                                                                                                                                                                                                                                                                                                                                     Local Similarity
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                                                                                                                                                                                                                                                                                          WNRGVPFRHLLLVLQLALLPAATOGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                                    TWTCTVLQNQKKVEFKIDIV
                                                                                                                                                                                                LVFGLTANSDTHLLQGQSLTLTLESSPGSSSSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                                                                 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                        TWTCTVLQNQKKVEFKIDIV
                                                                                                                                                                                    LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                                                                              ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFFLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                                                                            MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Banapour B,
                                                                                                                                                                                                                                                                                                                         78.1%; So. larity 100.0%; I Conservative 0;
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94US-00284391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ņ
                                                                                                                                                                                                                                                                                                                          Score 1029; DB 2;
Pred. No. 1.6e-63;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                Length 398;
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RESULT 25
AAR06374
ID AAR06
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AC AAR06
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                    This sequence represents the D1-D4 domains of CD4. This sequence is included in the membrane bound proteinaceous chimeric receptor of the invention. The extracellular portion of the chimeric receptor contains a fragment of CD4 (amino acids 1-394 or 1-200 of the CD4 sequence) which specifically recognises and binds HIV-infected cells, but does not mediate HIV infection. The extracellular domain of the receptor is separated from the cell membrane by 48 or 72 angstroms, or by one or more proteinaceous alpha-helices. The transmembrane region of the chimeric receptor contains a portion of the CD7, CD5 or CD34 transmembrane domain. Alternatively, the extracellular portion of the receptor can also be separated from the intracellular domain by the hinge, CH2 and CH3 domains of human IgG1. The cells expressing the receptor are preferably T cells, neutrophils, or dendritic cells. The therapeutic cells expressing the chimeric receptor are administered to a mammal to treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Membrane-bound chimeric receptor comprising extracellular portion including CD4 fragment - cells expressing receptor can be used for treatment of HIV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1996-129034/13.
N-PSDB; AAT10797.
           AAR06374;
                                 AAR06374 standard;
                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 10; Fig 23; 134pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-AUG-1994;
24-FEB-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CD7; transmembrane domain; chimeric receptor; CD5; CD34; CH2; CH3; IgG1; human; CD4; HIV; proteinaceous alpha-helix; T cell; B cell; neutrophil; dendritic cell; therapy; mammal; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human; CD4; HIV;
dendritic cell; t
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                                                                                                            181
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                                                                                                                                                                                                                                                                           200;
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                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GEN HOSPITAL CORP
                                                                                                                                                                                                                                          MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKS1QFHWKNSNQIK
                                                                                                                                                LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                            | ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                               TWTCTVLQNQKKVEFKIDIV 200
                                                                                                                                                                                                                              MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                                                                                                                                                                                                       398 AA;
                                                                                                                                   LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Banapour B,
                                                                                                                                                                                                                                                                         78.1%; Scilarity 100.0%; F
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95US-00394388.
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                                protein;
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                                                                                                                                                                                                                                                                         Score 1029; DB 2;
Pred. No. 1.6e-63;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                              Length 398;
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Best Local Signatches 200;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  soluble forms may be modified to increase their immunogenicity by addition of an adjuvant such as incomplete Freund's adjuvant. The T4 interferes with HIV/T4 interaction and elicits anti-soluble T4 antibody production. See also AAQ05607. (Updated on 31-OCT-2002 to add missing O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T4-encoding plasmid pBG381 was used to transform Chinese Hamster Ovary cells for the production of truncated T4. Soluble T4 is produced by virtue of the removal of the transmembrane and cytoplasmic domains. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1990-254040/33.
N-PSDB; AAQ05608.
                                                                                                                                                                                                                                                                                                                                                                             Sequence 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Treating or preventing AIDS, ARC or HIV infection - limmunologically effective amt. of soluble T4 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Region
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20-DEC-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HARD ) HARVARD
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181
                                   181
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                                                                                                                                                                                                                                                                                                                      Similarity
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                         TWTCTVLQNQKKVEFKIDIV
                                                                      LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                            LVFGLTANSDTHLLQGQSLTLTLESPPGSSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                        ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                                             MNRGVPFRHLLLVLQLALLLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                                 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                            MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of soluble T4 encoded by pBG381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             soluble T4 protein; AIDS; ARC; HIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= extracellular
/note= "homology to J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= secretory signal
/note= "hydrophobic"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                          78.1%; 5cc
100.0%; Pr
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                                                                                                                                                                                                                                                                                                  Score 1029; DB 2;
Pred. No. 1.6e-63;
0; Mismatches 0;
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RESULT 26
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31-OCT-2002
14-MAY-1990
                                                                                                                                                                                                                                 It may be capable of binding gp120. It may be fused with an immunoglobulin constant domain, human transferrin, apolipoprotein, albumin, ricin A chain or diphtheria toxin A. It may be used for antiviral of immunomodulatory therapy particularly in treatment of HIV infection. It may have variants by insertion, substitution of deletion in non-functional regions. (Updated on 1-0CT-2002 to add missing OS field.) (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to
                                                                                                                                                                                                                                                                                                                                                              Compsns. contg. adheson variants - useful in therapy and diagnostics, e.g. CD4 variants which are therapeutically useful for treating human immuno-deficiency virus.
                                                                                                                                                                                                Sequence 402 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1989-131855/18.
N-PSDB; AAN90777.
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28-SEP-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAP91922 standard; protein;
                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig la-1c; 36pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-OCT-1988;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence of a secreted form of the CD4 adhesion (CD4T) polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAP91922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GETH ) GENENTECH INC.
                                                                                                                                                         Local Similarity
121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
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                                                     ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                         MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                        ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                         MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gregrory TJ;
                                                                                                                                                                                                                         field.
                                                                                                                                             Conservative
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(revised)
(first en
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CD4T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87US-00104329
88US-00250785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88EP-00309194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "signal processing site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gp120; plasmid pRKCD4; HIV-1; HTLV-IIIB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entry)
                                                                                                                                                     78.1%;
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                                                                                                                                            0,
                                                                                                                                            Score 1029; DB 1;
Pred. No. 1.6e-63;
0; Mismatches 0;
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                                                                                                                                                                  Length 402;
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                                                                                                                                            Gaps
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1 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK

Matches

200;

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Mismatches

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Gaps

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ARESULT 27
AAP94757
ID AAP94
XX AAP94
XX AAP94
XX AAP94
XX Z3-M2
DT 25-M2
DT 28-J7
XX Seque
XX Homo
XX Homo
XX Homo
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XX O6-Al
XX O6-Al
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DR WPI;
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03-OCT-2002
28-JAN-1991
                                                                                                                                                      The patent claims a nucleic acid encoding an aa sequence variant of an adheson, which is pref. a CD4 polypeptide variant modified such that its transmembrane domain has been inactivated, either deleted or replaced by a sequence of hydrophilic hydropathy profile. The aa sequence variant of an adheson may also be a fusion of CD4 with a 2nd polypeptide esp. one contg. a non-CD4 epitope; a signal sequence; a cpd. able to elicit a humoral immune response (viral polypeptide or allergen); or a human plasma protein of long plasma half-life. CD4 fusion proteins can have antiviral and immunomodulatory activity and are esp. useful for treating HIV infections regardless of genetic variation within the virus. They and antibodies raised against them can also be used diagnostically for assaying adhesons and their ligands. (Updated on 03-OCT-2002 to add missing OS field.) (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB;
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                                                                                                       Sequence 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig la-1c; 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid sequences encoding adheson, esp. CD 4, partic. with trans-membrane domain inactivated or fused
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28-SEP-1988;
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                           Local Similarity
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DB; AAN90734.
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ilarity 100.0%;
Conservative (
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(revised)
(first entry)
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88US-00250785
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26. .402
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                      Score 1029; DB 1;
Pred. No. 1.6e-63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      infections
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RESULT 28
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WPI; 1988-064019/09.
N-PSDB; AAN80512.
                                                           21-AUG-1986;
                                                                         20-AUG-1987;
                                                                                                                                                           Region
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                                                                                                                                                                                                                                                                    Region
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                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                                                      Human Immunodeficiency Virus T4 envelope glycoprotein; AIDS; ss.
                                                                                                                                                                                                                                                                                                                                                                    Clone pT4B encoded HIV T4 glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                    25-MAR-2003
15-OCT-1990
                                                                                                                                                                                                                                                                                                                                                                                                                        AAP81990 standard; protein; 458
                     Littman DR,
                                   (UYCO-)
                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                 Peptide
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                                    MADDON P J.
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                    Maddon PJ,
                                                                                                                                                                                                                                                                                                                                                                                    (revised)
(first entry)
                                                           86US-00898587
                                                                          87WO-US002050
                                                                                                                                                   378. .39
/label=
                                                                                                                              /label= trans-membrane
421. .458
                                                                                                                                                                                         /label= putative N-glycosylation 310. .377
                                                                                                                                                                                                                                                                                                         /label
                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                      /label= variable-like region
288. .309
                                                                                                                      /label= cytoplasmic region
                                                                                                                                                                   label=
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                                                                                                                                                                                                                                                             'label= variable-like region
                                                                                                                                                                                                                                                                            'label= joining-like region 1
                                                                                                                                                                                                                                                                                          'label= variable-like region 1
                                                                                                                                                          el= putative N-glycosylation
_397
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                                                                                                                                            el= joining-like region 4
                                                                                                                                                                         le variable-like region 4
.327
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                     Chess L,
                     Axel R,
                                                                                                                                                                                                                                             region
                     Weiss R,
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                     Mcdougal
                      JS;
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RESULT 29
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25-MAR-2003
08-JAN-1990
                                                          Binding-site
Domain
Binding-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid encoding T4 glyco:protein - used for treatment of AIDS and producing antibodies for use as vaccine for immunisation against AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                   T4 protein encoded by part of 3kb insert from (pT4B). (Updated on 25-MAR-2003 to correct PA \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page ?; 128pp; English.
                                                                                                                                                   Domain
                                                                                                                                                                              Homo
                                                                                                                                                                                           T4 protein; human immunodeficiency virus; AIDS; clone pT4B
                                                                                                                                                                                                        T4 protein
                                                                                                                                                                                                                                                 AAP91369;
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                   EP330227-A.
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                                                                                                                                                                              sapiens;
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                                                                                                                                                                                                                                                                                                                                                                                                          h 78.1%; Sc. Similarity 100.0%; P
                                                                                                                                                                                                                                                             standard; protein;
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                                                                                                                                                                                                                                                                                                          TWTCTVLQNQKKVEFKIDIV 200
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(revised)
(first entry)
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                                                                                                                                                                              (human).
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135.
155
184
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287.
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                                                                                                                                                               Location/Qualifiers
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                                                                  .204 .286 .309 .298 .376
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Pred. No. 1.8e-63;
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field.
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30-AUG-1989

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RESULT 30
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AC AAR13
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Best Local Similarity
Matches 200; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74 protein (AAN90619) inhibits extracellular and cell-to-cell spread of HIV. The therapeutic agent consists of amino acids +3+185 fused to +351-+369; +3+106 fused to +351-+369; or +3+185. Also used to identify inhibitors of 74+ interactions, as target carrier proteins, and to generate monoclonal antibodies. Above features are: Domain 1 (D; starting at the N-terminal) = leader; D2 = variable-like-l; D3 = joining-like-l; D4 = V2; D5 = V3; D6 = J3; D7 = U3; D8 = J4; D9 = transmembrane; D10 = cytoplasmic; Regions are extracellular cysteines; and the 2 sites are potential N-linked glycosylation sites. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                               C4bp;
                                                                                                                                                                                                                                                                                                                                      25-MAR-2003
30-OCT-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 458 AA;
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(SMIK )
(UYCO )
                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                            Human CD4 encoded by pJOD.sCD4.Y187.SnaB1 and p170.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR13491 standard; protein; 458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                                                               gp120; HIV; T lymphocyte;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ΡJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMITHKLINE BECKMAN CORP. UNIV COLUMBIA NEW YORK. UNIV COLUMBIA NEW YORK.
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d of HIV used
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                                                                                                                                                                                                                                                                                                                                   (revised)
(first entry)
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                                                                     1. .25
/label= signal_peptide
                                                                                                                            Location/Qualifiers
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                       Ig-related
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Pred. No. 1.8e-63;

    inhibitors of extracellular and
vention and treatment of AIDS.

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ID AAY39
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AAY39826;

AAY39826 standard;

protein;

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Best Local
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                                                                                                                                                                                                                proteins with C4-binding protein. Truncated, soluble versions of CD4 can also be used. The C4bp-CD4 fusion protein may be useful to target AZT or similar anti-retroviral agent to HIV-infected cells. See AAQ13242-51. (Updated on 25-WAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                      New C4 binding protein fusion proteins and DNA encoding them - comprise assemblies of C4bp monomers linked to functional moiety, e.g. AZT, useful as delivery vehicles in diagnosis and therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disulfide-bond
Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disulfide-bond
Domain
                                                                                                                                                                                                      Sequence 458
                                                                                                                                                                                                                                                                                    Example 3; Fig 3; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAQ13243.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-AUG-1991.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Domain
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                                                                                                                                                                                                                                                                                                                                                          WPI; 1991-252613/34.
                                                                                                                                                                                                                                                                                                                                                                              Pasek MP,
                                                                                                                                                                                                                                                                                                                                                                                                                      26-JAN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                          26-JAN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9111461-A
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                                                                                                                                 1 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                                                         Similarity
                                      ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
             TWTCTVLQNQKKVEFKIDIV 200
                                                                               ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                      MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                                                                                                                                                                                                                                                             Winkler G,
                                                                                                                                                               Conservative
                                                                                                                                                                                                      AA;
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417. .456
/label= cvr~~~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "extracellular"
155. .184
203. .318
/label= ig-related
/note= "extracellular"
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396. .416
/label= tr
417. .456
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/note= "extracellular"
                                                                                                                                                                      78.1%;
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                                                                                                                                                           Score 1029; Db 4;
Pred. No. 1.8e-63;
Pred. No. 1.8e-63;
                                                                                                                                                                                  Length
                                                                                                                                                               Indels
                                                                                                                                                                                   458;
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RESULT 32
AAB07769
ID AAB077
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XX Humar
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Matches 200
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11-JUN-1991;
06-JUL-1992;
        Human; T4 glycoprotein; human immunodeficiency virus; HIV; envelope glycoprotein; AIDS; virus binding.
                                                                                                                                                                                                                                                                                                                                                                             This sequence represents the soluble human T4 protein of the invention. The soluble human T4 protein blocks the binding of HIV to T4+ cells and is therefore useful for the treatment of AIDS. Monoclonal antibodies against the T4 protein may be used as vaccines for immunising subjects
                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Soluble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Soluble human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-DEC-1999
                                     DNA encoding a human
                                                         07-NOV-2000
                                                                                                AAB07769
                                                                                                                                                                                                                                                                                                                                                                                                                                 Example
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                                                                                                                                                                                                                                                                                                                                                   458
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immunisation; therapy.
                                                                                                standard;
                                                                                                                                                              TWTCTVLQNQKKVEFKIDIV
                                                                                                                                                                                                   LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                                                             ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                                         ILGNQGSFLTKGPSKLNDRADSRRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
                                                                                                                                                                                                                                                                    MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein inhibits
                                                                                                                                                 TWTCTVLQNQKKVEFKIDIV
                                                                                                                                                                                       LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
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larity 100.0%;
Conservative
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91US-00713564.
92US-00909021.
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                                                                                              protein;
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                                                         entry.
                                   T4 glycoprotein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          HIV binding
                                                                                                                                                                                                                                                                                                          Score 1029; DB 2;
; Pred. No. 1.8e-63;
0; Mismatches 0;
                                                                                                458
                                                                                                                                                                   200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  binding inhibitor;
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Matches 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid encoding a human T cell surface protein and soluble surface T4 glycoprotein that it encodes, useful as prophylaxis for treating a subject infected with human acquired immune deficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-505203/45.
N-PSDB; AAA59352.
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12-DEC-1994;
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11-JUN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Domain
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                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig
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                                                                                                                                                                                                                                   458
     TWTCTVLQNQKKVEFKIDIV
                              LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                            LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                             MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                                                                                                                                                                                                                                                                                                                       virus.
                                                                               ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                            ILGNQGSFLTKGPSKLNDRADSRRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                                                               78.1%; llarity 100.0%; Conservative C
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91US-00713564.
92US-00909021.
94US-00354452.
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.458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "leader
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "cytoplasmic
                                                                                                                                                                               Score 1029; DB 3; pred. No. 1.8e-63; 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                             English.
      200
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RESULT 33
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Matches 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Therapeutic cells expressing chimeric receptors - directing cellular response to an infective agent, useful in treating HIV-1, AIDS Pneumocystis carinii infections etc.
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28-JUL-1995
                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               extracellular domain; mouse; human; receptor; HPB-ALL tumour cell line; natural killer cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fusion protein; CD4; extracellular domain; zeta; eta; gamma; membrane spanning domain; intracellular domain; type I; integral membrane homodimer; TCR; T cell antigen receptor; extracellular domain; mouse; human; receptor; chimera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CD4:eta peptide
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                                                                                                   Local Similarity
les 200; Conserv
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                                                   MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                                                  462
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 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                                                                                                                                                                                                                                                                                                                               Page 73-74; 114pp; English.
                                                                                                   Conservative
                                                                                                                                                                  Α
Α
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                400.
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1. .399
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                                                                                                                 78.1%; Score 1029; DB 2; 100.0%; Pred. No. 1.9e-63;
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Best Local
                                                                                                                                                                                                           Sequence 462 AA;
                                                                                                                                                                                                                                            Fusion proteins comprising the extracellular domain of CD4 fused to T-cell receptor zeta, gamma or eta (AAR78676-78, respectively) were expressed in CVI using a vaccine virus vector. These CD4:zeta, CD4:gamma and CD4:eta chimeric receptors mediated cytolysis of targets expressing
                                                                                                                                                                                                                                                                                                                                                             WPI; 1995-292893/38.
P-PSDB; AAQ96123.
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                                                                                                                                                                                                                                                                                                     Example
                                                                                                                                                                                                                                                                                                                                     Target cytolysis of HIV-infected cells
                                                                                                                                                                                                                                                                                                                                                                                                                                            14-FEB-1994;
02-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chimeric receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T-cell receptor gamma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR78677;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR78677
                                                                                                                                                                                                                                HIV gp120/41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9521528-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human
                                                                                                                                                                                                                                                                                                                                                                                                                      (GEHO ) GEN HOSPITAL CORP.
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 181
                                                                     61
                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ric receptor; CD4; T-cell receptor gamma; HIV; cytolysis; immunodeficiency virus; adoptive immunotherapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
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                                                                                                                                                                                                                                                                                                     <u>ب</u>
                                                                                                                                                                           Similarity
                                    LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                              MNRGVPFRHLLIVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TWTCTVLQNQKKVEFKIDIV 200
                     LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                    ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                                                                                                                                                                                                                                                                              Banapour B,
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                                                                                                                                                                                                                                                                                                     Page 77-78; 118pp; English.
                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first
                                                                                                                                                                                                                                                                                                                                                                                                                                           94US-00195395.
94US-00284391.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein; 462
                                                                                                                                                                       78.1%;
                                                                                                                                                                                                                                                                                                                                                                                                Romeo
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                                                                                                                                                            Score 1029; DB 2;
; Pred. No. 1.9e-63;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                        chimeric
                                                                                                                                                                                   Length 462;
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                                                                                                                                                                                                                                                         CD4:gamma
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RESULT 35
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ID AAR89
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XX AAR89
XX AAR89
XX CD7;
KW CD7;
CC CEHC
XX CEHC
XX CEHC
XX CENT;
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Matches 200
                                                                                                                                                                                                                                                                                                                                                                                                                   portion of the CD7 (see AAR89440), CD5 or CD34 transmembrane domains. Alternatively, the extracellular portion of the receptor can be separated from the intracellular domain by the hinge, CH2 and CH3 domains of human IgG1 (see AAR89441). The extracellular portion of the chimeric receptor contains a fragment of CD4 (amino acids 1-394 or 1-200 of the CD4 sequence, see AAR89450 and AAR89451) which specifically recognises and binds HIV-infected cells, but does not mediate HIV infection. The extracellular domain of the receptor is separated from the cell membrane by 48 or 72 angstroms, or by one or more proteinaceous alpha-helices. The cells expressing the receptor are preferably T cells, B cells, neutrophils, or dendritic cells. The therapeutic cells expressing the chimeric receptor are administered to a mammal to treat HIV infection
                                                                                                                                                                                                                                                                                                                                                                   Sequence 462 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAT10801-T10803 represent membrane bound proteinaceous chimeric receptors of the invention. This sequence represents the CD4:gamma chimera. The transmembrane region of the chimeric receptor acts to separate the intracellular and extracellular domains of the chimera, and contains a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Membrane-bound chimeric receptor comprising extracellular portion including CD4 fragment - cells expressing receptor can be used for treatment of HIV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CD4:gamma
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24-FEB-1995;
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                                                                                                                                                                                                                                                                         ocal Similarity
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                                      ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
                                                                                                                                                      MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKS1QFHWKNSNQIK
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ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                   MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
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95US-00394388
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100.0%; Pr
0;
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Pred. No. 1.9e-63;
0; Mismatches 0;
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       engineered form of the CD4 cellular receptor for HIV and the transmembrane and intracellular regions, including the cytolytic signal-transducing portion, of the human Fc receptor gamma chain; the region of the fusion is shown in AAW02223. It can be obtd. by inserting a gene fusion (AAT36759) into a vaccinia virus vector and expression in host cells. Chimaeric receptors comprising CD4 fused to Fc receptor gamma or Tecal receptor zeta (see also AAW02213) or eta (AAW02215) chains are capable of directing cycotoxic T lymphocytes to specifically recognise and kill cells expressing HIV gp120, thus providing a therapy for AIDS
                                                                                                                                                                                                         chimaeric receptors - co
                                                                                                                                                                                                                       Direction of cellular immune response using therapeutic cell expressing chimaeric receptors - comprising region binding to target cell and region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chimaeric receptor; cellular immunity; adoptive immunotherapy; CD4; human immunodeficiency virus type 1; HIV-1; AIDS; therapy; Fc receptor gamma chain; cytotoxic T lymphocyte; CTL.
                                                                                                                                       A chimaeric receptor (AAW00214) comprises the extracellular domain of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Regior
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW02214;
                                                                                                                                                                  Claim 7; Page 76; 120pp; English.
                                                                                                                                                                                            eliminating HIV-infected
                                                                                                                                                                                                                                                                                  WPI; 1996-402134/40
                                                                                                                                                                                                                                                                                                            Seed B,
                                                                                                                                                                                                                                                                                                                                                                    24-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                25-JAN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CD4:Fc receptor
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                                                                                                                                                                                                                                                                                                                                        (GEHO)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gamma chain chimaeric receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "region of fusion derived from gamma chain preferred signal-transducing portions for constructhe invention are amino acids 421-462 and 402-419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "encoding DNA contains a BamHI site used
fusion construction"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= Transmembrane+Intracellular_domains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                194. .397
/label= Linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         label= Extracellular_domain
                                                                                                                                                                                                                                                                                                            Kolanus
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                                                                                                                                                                                               cells.
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RESULT 37
AAW83142
ID AAW83
XX AAW83
XX Chime
XX Chime
XX Chime
XX Human
KW Lumou
KW CD4;
KW Proto
OS Synth
OS Mus s
XX PN US584
XX O1-DE
XX O1-DE
XX O1-DE
XX O1-BE
XX O1-ME
PF 05-AI
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Best Local (
                                                                                                                                                                                                                                                                                                                                                           07-MAR-1991;
06-MAR-1992;
28-FEB-1994;
         The present invention describes DNA encoding a membrane-bound chimeric receptor comprising: (a) an extracellular portion that specifically recognises and binds a target cell or a target infective agent; and (b) an intracellular portion of a T-cell receptor CD3, zeta or eta polypeptide, a B-cell receptor polypeptide or an Fc receptor polypeptide. The present sequence represents a chimeric receptor containing the mouse gamma polypeptide. Cells expressing chimeric receptors of the present invention can be administered to mammals in order to destroy pathogens.
                                                                                                                                                                                     Membrane-bound chimeric receptors - which recognises and binds a target e.g. a T-cell receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; zeta; eta; gamma; membrane-bound chimeric receptor; infection; tumour; cancer cell; autoimmune-generated cell; T cell receptor; CD3; CD4; B cell receptor; Fc receptor; pathogen; bacterial; fungal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                         Example
                                                                                                                                                                                                                                                                                                 Romeo
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                                                                                                                                                                                                                                                                                              Kolanus W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  viral.
                                                                                                                                                      Col 43-46; 57pp; English.
                                                                                                                                                                                                                                                                                                                              HOSPITAL
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92US-00847566.
94US-00203866.
                                                                                                                                                                                                                                                                                                                                                                                                                         95US-00417495
fungi, protozoa or viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         containing
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Pred. No. 1.9e-63;
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especially
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RESULT 38
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Best Local S
Matches 200
 This sequence represents a fusion protein between the CD4 extracellula domain and the gamma protein membrane spanning domain and intracellula domain and the Fc-receptor-associated gamma chain is expressed in cell surface complexes with additional polypeptides, some of which mediate ligand recognition, and others which have undefined function. Gamma be a homodimeric structure and overall organisation very similar to that zeta (see also AAQ28704), and is a component of both the mast cell/basophil high affinity IgE receptor, Fc-epsilon-RI, which consist
                                                                                                                                                                                                                                           Seed
zeta (see aısc
cell/basophil
                                                                                                                                                            Therapeutic cells expressing chimeric receptors - cresponse to an infective agent, useful in treating
                                                                                                                                                                                                   WPI; 1992-331474/40.
N-PSDB; AAQ28706.
                                                                                                                                                                                                                                                                                                                                                                                                                                       membrane spanning domain; intracellular domain; type I; integral membrane homodimer; TCR; T cell antigen recept extracellular domain; mouse; human; receptor; chimera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or autoimmune-generated
                                                                                                                      Example 2; Page 74-76; 114pp; English.
                                                                                                                                                                                                                                                                                             07-MAR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fusion protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CD4:gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-MAR-2003
28-JUL-1995
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                                                                                                                                                 Pneumocystis carinii infections etc.
                                                                                                                                                                                                                                                                                                                       06-MAR-1992;
                                                                                                                                                                                                                                                                                                                                                17-SEP-1992.
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                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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                                                                                                                                                                                                                                                                   (GEHO)
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                                                                                                                                                                                                                                         Romeo C,
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                                                                                                                                                                                                                                                                                             91US-00665961
                                                                                                                                                                                                                                                                                                                       92WO-US001785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CD4; extracellular domain;
                                                                                                                                                                                                                                         Kolanus W;
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g HIV-1, AIDS
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Best Local
cell receptor zeta, gamma or eta (AAR78676-78, respectively) were expressed in CVI using a vaccine virus vector. These CD4:zeta, CD4 and CD4:eta chimeric receptors mediated cytolysis of Franciscus, CD4 HIV gp120/41
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                                                                                                                                                            Example
                                                                                                                                                                                                                                 Target
                                                                                                                                                                                                                                                                                  WPI; 1995-292893/38.
N-PSDB; AAQ96124.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-FEB-1994;
02-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chimeric receptor; CD4; T-cell receptor eta; HIV; cytolysis; human immunodeficiency virus; adoptive immunotherapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T-cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-JAN-1995;
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                                                                                                                                                                                                                                 cytolysis of HIV-infected cells -
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                                                                                                                                                                                                                                                                                                                                                       Banapour B,
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94US-00284391.
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Pred. No. 2.2e-63;
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                                                                                                                                                                                                                                                                                                                                                          Kolanus
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ARRESULT 40
AAR89458
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XX 26-SE
XX CD7;
KW CD7;
KW CD7;
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XX 15-FE
XX 02-AU
PR 24-FE
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             AAT10801-T10803 represent membrane bound proteinaceous chimeric receptors of the invention. This sequence represents the CD4:eta chimera. The transmembrane region of the chimeric receptor acts to separate the intracellular and extracellular domains of the chimera, and contains a portion of the CD7 (see AAR89440), CD5 or CD34 transmembrane domains. Alternatively, the extracellular portion of the receptor can be separated from the intracellular domain by the hinge, CH2 and CH3 domains of human 1gG1 (see AAR8941). The extracellular portion of the chmeric receptor contains a fragment of CD4 (amino acids 1-394 or 1-200 of the CD4 sequence, see AAR8945) and AAR89451) which specifically recognises and
                                                                                                                                                                                                                                                                                                                                                                        Membrane-bound chimeric receptor comprising extracellular portion including CD4 fragment - cells expressing receptor can be used for treatment of HIV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CD7; transmembrane domain; chimeric receptor; CD5; CD34; CH2; CH3; IgG1; human; CD4; HIV; proteinaceous alpha-helix; T cell; B cell; neutrophil;
sequence, see AAR89450 an
binds HIV-infected cells,
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24-FEB-1995;
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                                                                                                                                                                                                                                                                                                                      Page 80-81; 134pp;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                               Chimaeric receptor; cellular immunity; adoptive immunotherapy; CD4; human immunodeficiency virus type 1; HIV-1; AIDS; therapy; T-cell receptor eta chain; cytotoxic T lymphocyte; CTL.
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11-NOV-1996
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(first entry)
96WO-US001056
                                                                                                                                                  /note= "region of fusion derived from eta chain, preferred signal-transducing portions for constructs the invention are amino acids 421-532, 423-455, 438-4461-494, 494-528 or 400-420"
                                                                                                                                                                                                       397
                                                                                                                                                                                                                 /note= "encoding DNA fusion construction"
                                                                                                                                                                                                                                                                 /label= Extracellular_domain
/note= "CD4 extracellular dom
                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                             /label= Transmembrane_domain
/note= "eta chain transmembr
                                                                         'note= "eta chain intracellular
                                                                                                                                                                                                                                          'label= Linker
                                                                                                                                                                                                                                                       .396
                                                                                                  . 575
                                                                                      Intracellular_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1029; DB 2;
Pred. No. 2.2e-63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                              contains
                                                                                                                                                                                                                                                                   domain"
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                                                                          domain'
                                                                                                                                                                                                                              BamHI site used
                                                                                                              domain"
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                                                                                                                                                                 438-455
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RESULT 42
AAW83141
ID AAW83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transmembrane and intracellular regions, including the cytolytic signal-transducing portion, of the mouse T-cell receptor eta chain. It can be obtd. by inserting a gene fusion (AAT36760) into a vaccinia virus vector and expression in host cells. Chimaeric receptors comprising CD4 fused to eta, eta (see also AAW02213) or Fc receptor gamma (see also AAW02214) chains are capable of directing cytotoxic T lymphocytes to specifically recognise and kill cells expressing HIV gp120, thus providing a therapy for AIDS. (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direction of cellular immune response using therapeutic cell expressing 2 chimaeric receptors - comprising region binding to target cell and region that signals target cell destruction, or CD28 region, partic. for eliminating HIV-infected cells.
                                                                                                                        Human; zeta; eta; gamma; membrane-bound chimeric receptor; tumour; cancer cell; autoimmune-generated cell; T cell receCD4; B cell receptor; Fc receptor; pathogen; bacterial; fur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A chimaeric receptor (AAW00215) comprises the extracellular domain of engineered form of the CD4 cellular receptor for HIV and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 7; Page 77-78; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seed
                                                                                                            protozoan; viral.
                                                                                                                                                                                Chimeric receptor containing
                                                                                                                                                                                                              03-FEB-1999
                                                                                                                                                                                                                                          AAW83141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAT36760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1996-402134/40.
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                                        US5843728-A.
                                                                                 Synthetic
                                                                                                                                                                                                                                                                    AAW83141 standard;
                                                                    Omo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            532 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                            LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Romeo
                                                                                                                                                                                                                                                                                                                                                                   TWTCTVLONOKKVEFKIDIV
                                                                                                                                                                                                                                                                                                                                                                                                  LVFGLTANSDTHLLQGQSLTLTLESPPGSSPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78.1%; ilarity 100.0%; Conservative
                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ú
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                                                                                                                                                                                                                                                                   protein;
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                                                                                                                                                                                                                                                                    532
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1029; DB 2;
Pred. No. 2.2e-63;
0; Mismatches 0;
                                                                                                                                                                                human eta polypeptide.
                                                                                                                                                                                                                                                                                                                                                                     200
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                                                                                                                                                                                                                                                                                                                                                                                                 VQCRSPRGKNIQGGKTLSVSQLELQDSG
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                                                                                                                                      infection;
eptor; CD3;
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RESULT 43
AAR27276
ID AAR27
XX AAR27
XX AAR27
XX 25-MA
DT 25-MA
DT 28-JU
XX CD4:z
CDE CD4:z
XX Fusio
KW membx
KW integ
KW integ
KW extra
KW HPB-A
XX
XX
XX
HOMO
XX
XX
FH Key
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Best Local
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06-MAR-1992;
28-FEB-1994;
                                                    Fusion protein; CD4; extracellular domain; zeta; eta; membrane spanning domain; intracellular domain; type I integral membrane homodimer; TCR; T cell antigen recepextracellular domain; mouse; human; receptor; chimera; HPB-ALL tumour cell line; natural killer cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes DNA encoding a membrane-bound chimeric receptor comprising: (a) an extracellular portion that specifically recognises and binds a target cell or a target infective agent; and (b) an intracellular portion of a T-cell receptor CD3, zeta or eta polypeptide, a B-cell receptor polypeptide or an Fc receptor polypeptide. The present sequence represents a chimeric receptor containing the human eta polypeptide. Cells expressing chimeric receptors of the present invention can be administered to mammals in order to destroy pathogens (e.g. bacteria, fungi, protozoa or viruses, especially HIV), cancer cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Membrane-bound chimeric receptors - which recognises and binds a target e.g. a T-cell receptor.
                                                                                                                                                                                                                                            AAR27276
                           Homo sapiens
                                                                                                                                         CD4:zeta peptide chimeric protein
                                                                                                                                                                        25-MAR-2003
28-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-APR-1995;
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DB; AAV70157.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                532
                                                                                                                                                                                                                                            standard;
                                                                                                                                                                                                                                                                                                                                        TWTCTVLQNQKKVEFKIDIV
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                                                                                                                                                                                                                                                                                                                     TWTCTVLQNQKKVEFKIDIV
                                                                                                                                                                                                                                                                                                                                                                             LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                    ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kolanus W,
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                                                                                                                                                                     (revised)
(first entry)
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92US-00847566.
94US-00203866.
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Location/Qualifiers
                                                                                                                                                                                                                                            protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1029; DB 2;
Pred. No. 2.2e-63;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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                                                                                             eta; y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 532;
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AAR78676 standard; protein;

575

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16-APR-1996 T-cell rece

receptor

zeta.

(first

Chimeric receptor; CD4; T-cell receptor zeta; HIV; c human immunodeficiency virus; adoptive immunotherapy

HIV; cytolysis;

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                                                                                                                                                                                                                                                                               Matches
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Best Local
                                                                                                                                                                                                                                                                                                      domain. Zeta is a 32 kD type I integral membrane homodimer which has a 9 residue extracellular domain and a 112/113 residue intracellular domain for mouse and human protein respectively. In the production of the CD4 receptor chimera, the zeta cDNA was isolated from the HPB-ALL tumour cell line and from human natural killer cells. The zeta cDNA was joined to the extracellular domain of an engineered form of CD4 possessing a BamHI site just upstream of the membrane spanning domain, by a BamHI site naturally present a few residues upstream of the membrane spanning domain. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Therapeutic cells expressing chimeric receptors - directing ce response to an infective agent, useful in treating HIV-1, AIDS Pneumocystis carinii infections etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seed
                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 2; Page 72-73; 114pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-SEP-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9215322-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence represents a 
in and the zeta proteir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1992-331474/40.
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 181
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                                                                               121
                                                                                                                                                                                                                        200;
                                                                                                            19
                                                                                                                                      13
                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                               575
              TWTCTVLQNQKKVEFKIDIV 200
                                                      LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                     LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKN1QGGKTLSVSQLELQDSG
                                                                                                                         ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Romeo
TWTCTVLQNQKKVEFKIDIV
                                                                                                            ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLTIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                   MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                               A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "CI
400. .575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Zeta membrane spanning and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kolanus
                                                                                                                                                                                                                                                                                                                                                                                                                                protein membrane spanning domain and intracellular
                                                                                                                                                                                                                                  78.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "CD4 extracellular domain"
                                                                                                                                                                                                                     Score 1029; UB 4,
Pred. No. 2.4e-63;
                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        intracellular domain"
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RESULT 45
AAR89456
ID AAR89
XX AR89
XX AR89
XX CD7:
CD4:2
XX CD7;
XW human
XW dendx
XX Synth
XX Synth
XX W0960
XX W9960
PD 15-FE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Target cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fusion proteins comprising the extracellular domain of CD4 fused to T-cell receptor zeta, gamma or eta (AAR/8676-78, respectively) were expressed in CV1 using a vaccine virus vector. These CD4:zeta, CD4:gamma and CD4:eta chimeric receptors mediated cytolysis of targets expressing
                                                                                          CD7; transmembrane domain; chimeric receptor; CD5; CD34; CH2; CH3; IgG1; human; CD4; HIV; proteinaceous alpha-helix; T cell; B cell; neutrophil;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-FEB-1994;
02-AUG-1994;
                                   WO9603883-A1
                                                        Synthetic
                                                                               dendritic
                                                                                                                             CD4:zeta fusion protein.
                                                                                                                                                     26-SEP-1996
                                                                                                                                                                                                  AAR89456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 575 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 2; Page 76-77; 118pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9521528-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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                                                                                                                                                                                                                                                                                   181
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                                                                                                                                                                                                                                                                                                                                                                                                    μ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cytolysis of HIV-infected cells -
                                                                                                                                                                                                                                                                                                                                                                                                                                                            h 78.1%;
Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAQ96122
                                                                                                                                                                                                                                                                                                                       LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                                                                                                                                                                                                                                                   MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                                                                                 standard;
                                                                                                                                                                                                                                                                        TWTCTVLQNQKKVEFKIDIV 200
                                                                                                                                                                                                                                                                                                                                                                                                   MRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Banapour B,
                                                                                                                                                                                                                                                                                                         LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                                                                                                                                                                                       ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                                                                                                                                                                       ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                                                            TWTCTVLQNQKKVEFKIDIV 200
                                                                                cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HOSPITAL
                                                                                                                                                    (first entry)
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94US-00284391.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95WO-US000454
                                                                              therapy; mammal;
                                                                                                                                                                                                 protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Romeo C,
                                                                                                                                                                                                  575
                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1029; DB 2;
Pred. No. 2.4e-63;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kolanus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             by chimeric CD4 receptor-bearing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 575;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAT10801-T10803 represent membrane bound proteinaceous chimeric receptors of the invention. This sequence represents the CD4:zeta chimera. The transmembrane region of the chimeric receptor acts to separate the cransmembrane region of the chimera receptor acts to separate the cransmembrane region of the chimera receptor acts to separate the cransmembrane and extracellular domains of the chimera, and contains a portion of the CD7 (see AAR89440), CD5 or CD34 transmembrane domains. Alternatively, the extracellular portion of the receptor can be separated from the intracellular domain by the hinge, CH2 and CH3 domains of human CC [361 (see AAR89441). The extracellular portion of the chimeric receptor contains a fragment of CD4 (amino acids 1-394 or 1-200 of the CD4 sequence, see AAR89450 and AAR89451) which specifically recognises and binds HIV-infected cells, but does not mediate HIV infection. The cutracellular domain of the receptor is separated from the cell membrane CC by 48 or 72 angstroms, or by one or more proteinaceous alpha-helices. The cells expressing the receptor are preferably T cells, B cells, CC cells expressing the receptor are preferably T cells, B cells expressing the receptor are preferably T cells and the cell membrane CC cells expressing the receptor are preferably T cells and the cell sexpressing the receptor are preferably T cells and T cells expressing the cells can be administered to a mammal to treat HIV infection or the content of the content o
                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 575 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Membrane-bound chimeric receptor comprising extracellular portion including CD4 fragment - cells expressing receptor can be used for treatment of HIV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-JUL-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Page 77-78; 134pp; English.
                                                                                                                                                              LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                            TWTCTVLQNQKKVEFKIDIV 200
                                                                                                                                                                                                                                                 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
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                                                                                                                                                                                                                 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                                                                                                                          MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94US-00284391.
95US-00394388.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             78.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Romeo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'n
                                                                                                                                                                                                                                                                                                                                                                                                                                   <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1029; DB 2;
Pred. No. 2.4e-63;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 575;
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60

180

120 120

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AAW02213
ID AAW02213
XX AAW02
XX AAW02
XY 11-NO
XX Chima
KW Chima
KW human
KW T-cel
XX T-cel
XX Homo
                                                                                         AAW02213 standard;
                                                            11-NOV-1996
                                                                           AAW02213;
                                                           (first
                                                                                        protein;
                                                           entry)
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Chimaeric receptor; cellular immunity; adoptive immunotherapy; CD4; human immunodeficiency virus type 1; HIV-1; AIDS; therapy; T-cell receptor zeta chain; cytotoxic T lymphocyte; CTL. CD4:T-cell receptor zeta chain chimaeric receptor.

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Query Match
Best Local S
Matches 200
                                                                                                                                                                                                                                                                                                                                                                                                                             A chimaeric receptor (AAW00213) comprises the extracellular domain of an engineered form of the CD4 cellular receptor for HIV and the transmembrane and intracellular regions, including the cytolytic signal-transducing portion, of the human T-cell receptor zeta chain; the region of the fusion is shown in AAW02221. It can be obtd. by inserting a gene fusion (AAT36758) into a vaccinia virus vector and expression in host cells. Chimaeric receptors comprising CD4 fused to zeta, eta (see also AAW02215) or Fc receptor gamma (see also AAW02214) chains are capable of directing cytotoxic T lymphocytes to specifically recognise and kill cells expressing HIV gp120, thus providing a therapy for AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direction of cellular immune response using therapeutic cell expressing chimacric receptors - comprising region binding to target cell and region that signals target cell destruction, or CD28 region, partic. for eliminating HIV-infected cells.
                                                                                                                                                                                                                                                                                                                                                                                           Sequence 575 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1996-402134/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 7; Page 74-75; 120pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-JAN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GEHO)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Domain
                                                                                                                                                                                                                                                                                                                          ocal Similarity
181
                                        121
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                                                                                                                              61
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                                                                                                                                                                                                                                      MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
                                                                 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
TWTCTVLQNQKKVEFKIDIV 200
                                                                                                                                                  ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
                                                                                                                                                                                                               MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                        LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                            ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Romeo C,
                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95US-00394176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "region of fusion derived from zeta chain, preferred signal-transducing portions for constructs of the invention are amino acids 421-575, 423-255, 438-455, 461-494, 494-528, 400-420 and 421-462"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "CD4 extracellular domain" 394. 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "encoding DNA fusion construction"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= Linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "zeta chain intracellular domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= Extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kolanus W;
                                                                                                                                                                                                                                                                                                                          78.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transmembrane
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Pred. No. 2.4e-63;
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                                                                                                                                                                                                                                                                                                                                            Length
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                                                                                                                                                                                                                           receptor comprising: (a) an extracellular portion that specifically recognises and binds a target cell or a target infective agent; and (b) an intracellular portion of a T-cell receptor CD3, zeta or eta polypeptide, a B-cell receptor polypeptide or an Fc receptor polypeptide. The present sequence represents a chimeric receptor containing the human zeta polypeptide. Cells expressing chimeric receptors of the present invention can be administered to mammals in order to destroy pathogens (e.g. bacteria, fungi, protozoa or viruses, especially HIV), cancer cells or autoimmune-generated cells
                                                                                                                                                                                                                                                                                                                                                                                             Membrane-bound chimeric receptors - comprising extracellular portion which recognises and binds a target cell and an intracellular portion e.g. a T-cell receptor.
                                                                                                                                                                                                      Sequence 575
                                                                                                                                                                                                                                                                                                                                                                       Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Romeo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-MAR-1991;
06-MAR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                            The present invention describes DNA encoding a membrane-bound
                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-044582/04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-APR-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protozoan; viral.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CD4; B cell receptor; Fc receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chimeric receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               reta; eta; gamma; membrane-bound chimeric receptor; infection;
cancer cell; autoimmune-generated cell; T cell receptor; CD3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAV70156
LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
               LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
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                                                ILGNOGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                   MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kolanus W,
                                                                                                                                                                                                                                                                                                                                                                     Col 39-42; 57pp;
                                                                                                                                                   Conservative
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92US-00847566.
94US-00203866.
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                                                                                                                                                  Score 1029; DB 2;
Pred. No. 2.4e-63;
0; Mismatches 0;
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                                                                                                                                                                          Length 575;
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ARESULT 48
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31-OCT-2002
29-MAY-1990
                                                                                                                                                                                                                                                                                                                                                                                                           X = stop codon. The sequence was deduced from the cDNA insert of pBG183. Soluble T4 constructs may be produced by truncating this sequence to give fragments from position 400 to 799, removing the transmembrane and intracytoplasmic domains whilst retaining the extracellular region responsible for HIV binding. The sol. T4 is combined with an anti-viral agent such as AZT. See also AAQ03005. (Typis combined with an anti-viral missing OS field.) (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Combinations of soluble synergistic activity in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR04032 standard;
                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure;
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(BIOJ
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20-APR-1989;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Soluble T4;
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                          LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                  | ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                                                                                             MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
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  LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                     ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
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                                                                                                                                                                                                                                                                      78.1%; So ilarity 100.0%; I Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T4 encoded by plasmid
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89US-00341080
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                                                                                                                                                                                                                                                                   Score 1029; DB 2;
Pred. No. 9.7e-63;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                   Length 2037;
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RESULT 45
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Best Local Similarity
Matches 200; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Entire sequence translation of plasmid pBG381 used to transform Chinese Hamster Ovary cells for the production of soluble truncated T4.

Transmembrane and cytoplasmic domain-encoding regions are deleted from the T4 CDS to encode a truncated protein. The soluble forms may be modified to increase their immunogenicity by addition of an adjuvant su as incomplete Freund's adjuvant. The T4 interferes with HIV/T4 interaction and elicits anti-soluble T4 antibody prodn. See also AAQ05607. (Updated on 31-OCT-2002 to add missing OS field.)
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20-DEC-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2050
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Treating or preventing AIDS, ARC or HIV infection - by administering immunologically effective amt. of soluble T4 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Deduced sequence of pBG381 comprising truncated T4 glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR07641;
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                                                                                                                                                                                                          ILGNQGSFLTXGPSKLNDRADSRRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                          LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                                                                                                                 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
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                                                                                                                                                                                                                                                                                                            MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                          TWICTVLONOKKVEFKIDIV
                                                                          LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                               ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
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Conservative
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100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                    Score 1029; DB 2;
Pred. No. 9.8e-63;
0; Mismatches 0;
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RESULT 50
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Best Local S
Matches 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The human kappa light chain constant region is excised from the plasmid pCNkappa light and ligated to M13mpl8. The purified vector containing the kappa light chain constant region is then ligated to human CD4 cDNA. The cDNA is used to prepare an expression vector encoding the light chains of a CD4-IgG1 chimeric heterotetramer designated CD4-KLC-pRcCMV (ATCC 75194). (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CD4-gamma 1 chimeric heavy chain homo-dimer and its expression vector - for preventing and treating HIV infection useful as a diagnostic agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Beaudry
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28-JAN-1993
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DB; AAQ27832.
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                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              310
TWTCTVLQNQKKVEFKIDIVPRASALPAPPTGSALPDPQTASALPDPPAASALPAALAVI
                                                                                                               LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180
                                                                                                                                                                                                                                                                                 MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diagnostic
                                                                             LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                 ILGNOXXFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                                 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CD4-kappa chimeric light chain heterotetramer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Maddon PJ;
                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                              78.0%;
84.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                           Score 1027; DB 2;
Pred. No. 1.6e-63;
                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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RESULT 51
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                                                    comprising the radionuclide can be used to image HIV infected tissue, to calculate the stage of HIV infection or the efficacy of an anti-HIV treatment using the imaging technique and for determining the prognosis of an HIV infected subject. (Updated on 25-MAR-2003 to correct PN field
                                                                                                                                                              A tetramer comprising 2 IgG2 heavy chains or two CD4-IgG2 chimeric heavy chains and two kappa light chains or CD4-kappa light chains (AAR46680) linked to a non-peptidyl toxin or a gamma radiation-emitting radionuclide of low to moderate cytotoxicity. The resulting immunoconjugate comprising the toxin can be used to kill HIV infected cells and to treat HIV infected cells to reduce the population of HIV infected cells. It can also be used to reduce the likelihood of infection. The immunoconjugate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Non-peptidyl toxin or radionuclide and CD4-gamma 2 or CD4-IgG2 immuno:conjugates - used to kill HIV-infected cells and to image and stage HIV infection.
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Sequence
                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 4; 142pp; English
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08-AUG-1994
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Query Match Best Local Similarity

77.9**%**; 84.4**%**;

Score 1026.5; DB Pred. No. 3.2e-63;

2

Length

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RESULT 52
AAAP93506
ID AAAP93
XX AAP93
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The coding sequenc is derived from the published sequence of sT4. sT4 useful in the prevention and treatment of ADS by inhibiting spread of the virus. It can also be used as an inhibitor of T4+ cell function, a reagent for identifying inhibitors of T4+ cell interaction and to produce the contraction of the contraction and to produce the contraction and the contraction and
                                                                                                                                                                                                                                                       Purifying soluble recombinant T4 lymphocyte surface protein - from cell culture by adsorption on cation exchanger, elution and treatment with
                                                                                                                                                                                                                                                                                                                                                      WPI; 1989-124209/17
N-PSDB; AAN90763.
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                                                             The invention relates to antibodies or antibody fragments specifically binding to CD4-inducible epitope on Human immunodeficiency virus (HTV) envelope glycoprotein (Env) proteins. The antibody is useful for preparing a composition for treating or preventing HTV infection. The invention is used to prepare vaccines and is used in gene therapy. The present sequence is a sCD4 protein used in the exemplification of the
                                                                                                                                                                                                                                                               New isolated antibody or antibody fragment specifically inducible epitope on Human Immunodeficiency Virus (HIV) useful for preparing a composition for treating or preveinfection.
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Mismatches 0
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Best Local Similarity
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The signal sequence is attached downstream of the plasmid sequence encoding a secreted protein, which will then produce proteins covalently anchored to the cell surface in which they were produced. This can give rise to plasma membrane binding, enhanced purifiability, micelle formation etc. especially useful in the production of chimeric targeted drugs, to produce micellular or liposomal delivery systems or in enhanced purification and screening of cells, proteins or DNA libraries. (Updated
                                                                                                                                   Phosphatidyl-inositol linkage signalling DNA sequence - derived from lymphocyte function-associated antigen 3, used for prodn. of chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasmid T4/LFA-3/AD gene product with C-terminal encoding phosphatidylinositol (PI) linkage signaling sequence.
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09-JAN-2003
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                                                                                                Disclosure; Fig
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DB; AAQ06404.
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267. .295
/label= PI signal peptide
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Pred. No. 1.9e-63;
0; Mismatches 1
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Best Local
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09-JAN-2003
06-FEB-1991
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                                                                                                                                                                                                                                                                                                            Plasmid T4/LFA-3/2 gene product with C-terminal encoding phosphatidylinositol (PI) linkage signaling sequence.
                                  Disclosure;
                                                          Phosphatidyl-inositol linkage signalling llymphocyte function-associated antigen 3,
                                                                                     N-PSDB;
                                                                                              WPI; 1990-334849/44.
                                                                                                               Wallner BP;
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/label= LFA-3 gene product
267. .318
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                                53pp;
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The signal encoding a anchored to

al sequence is attached downstream of the Plasmid sequence a secreted protein, which will then produce proteins covato the cell surface in which they were produced. This can

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Best Local Similarity
Matches 199; Conserv
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11-JUN-1991;
06-JUL-1992;
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                                                               This sequence represents the soluble human T4 protein of the invention The soluble human T4 protein blocks the binding of HIV to T4+ cells and is therefore useful for the treatment of AIDS. Monoclonal antibodies
                                            against the T4 protein m
                                                                                                                                                                                                                                   Human T4
                                                                                                                                                                                                                                                                                                             WPI; 1999-561025/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-DEC-1994;
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CC This sequence represents the full length amino acid sequence of CC glycosylated sT4 glycoprotein. Human immunodeficiency virus (HIV) uses CC sT4 as a target receptor on T cells. The invention relates to CC glycosylated sT4 which functions by blocking the binding of HIV to T4 CC target cells, and can be used for the prophylaxis and treatment of AIDS CC patients. Administration of sT4 effectively inhibits the cell to cell CC spreading of HIV infection and also the fusion of HIV-infected T4 cells CC and non-infected T4 cells. The administration of T4 alleviates several CC symptoms associated with AIDS, and prevents the occurrence of new pathological changes. The sT4 glycoprotein is useful for the prophylaxis CC and treatment of patients with AIDS. It is also useful as a reagent to therapeutic agents or inhibitors of T4+ cell interactions and in CC diagnostic assays for detection T4 proteins or malcules which act as
           RESULT 57
AAY88 328
ID AAY88 328
XX AAY88 328
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AIDS; treatment; inhibit; cell to cell spread; infection; fusion.
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Pred. No. 4.1e-63;
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Best Local Simi
Matches 199;
                                                                                                                                                                                                                                                                                                                                                                              22-JAN-1988;
23-JAN-1989;
09-JUN-1992;
12-APR-1993;
      The present sequence is that of fusion protein CD4Mmu comprising the extracellular portion of CD4, which binds to HIV gp120, linked at itt terminus to the human IgM heavy chain. To obtain the fusion protein, encoding CD4 was linked to IgM DNA at the Mst2 site upstream of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CD4 - IgM
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                                                                                                                                                                        CD4-immunoglobulin
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89US-00299596.
92US-00896781.
93US-00057952.
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                                                                                                                                                                          fusion
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                                                                                                           English
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Matches 199
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23-JAN-1989;
09-JUN-1992;
12-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 region (see AAA50662). Fusion protein CD4Mmu and a nucleic acid encoding it are claimed. Also claimed are a vector comprising the nucleic acid, and a method of producing the fusion protein in secreted form using a transformed host cell. The fusion protein may further comprise a therapeutic agent, radiolabel or NMR imaging agent. The fusion protein can be administered to an animal (including humans) for treatment of HIV or SIV infection, and can also be used in assays for HIV or SIV, imaging and tissue stains. IgM fusion proteins such as CD4Mmu provide complement-mediated immunity
                                                                                                Seed
                                                                  WPI; 2000-085792/07.
N-PSDB; AAZ44063.
                                                                                                                                                                                                                                                   Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                                                                 Fusion protein; anti-human immur
                                                                                                                                                                                          04-FEB-1994;
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                                               Fusion
                                                                                                                                                                                                                                 US6004781-A
                                                                                                                                                                                                                                                                                                                Human fusion
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                                                                                                                                                                                                                                                                                                                                                                          AAY51080 standard; protein;
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                                                                                                                                                                                                                                                                               tein; human; CD4; IgM; immunoglobulin; immunodeficiency virus; CD4Mg.
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93US-00057952.
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                                               for the treatment
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                                                human
                                               immunodeficiency virus.
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This invention describes protein comprising a DNA

a novel nucleic ac sequence encoding

acid (I) encoding a ng amino acids 1-173

fusion of CD4

(II)

Example

1;

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41-50;

39pp;

English

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Query Match
Best Local Sim.
Matches 199;
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This sequence represents the amino acid sequence of glycosylated sT4 glycoprotein. Human immunodeficiency virus (HTV) uses sT4 as a target receptor on T cells. The invention relates to glycosylated sT4 which functions by blocking the binding of HTV to T4 target cells, and can be used for the prophylaxis and treatment of AIDS patients. Administration of sT4 effectively inhibits the cell to cell spreading of HTV infection and also the fusion of HTV-infected T4 cells and non-infected T4 cells.
                                                                                                                                                                       Soluble T4 glycoprotein useful for prevention immunodeficiency syndrome and for screening ir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                             Example;
                                                                                                                                                        immunodeficiency
                                                                                                                                                                                                                                                                                  (UYCO ) UNIV COLUMBIA NEW YORK.
                                                                                                                                                                                                                                                                                                                 21-AUG-1986;
                                                                                                                                                                                                                                                                                                                                              23-OCT-1987;
                                                                                                                                                                                                                                                                                                                                                                             30-JUN-1992
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                                                                                                                                                        syndrome and for viral binding.
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99.5%;
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4.6e-63;
hes 1;
                                                                                                                                                                                                                                                    Littman
                                                                                                                                                                        inhibitors
                                                                                                                                                                                                                                                    DR,
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                                                                                                                                                                        treatment of acquired itors of human
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RESULT 61
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Best Local Sim
Matches 199;
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                                                                                                                                                                                                                                                                                                                                 Human; CD4; CD4 fusion protein; oligomerisation; receptor-ligand interaction inhibition; surface plasmon resonance; T cell receptor binding; MHC binding; carcinoma; autoimmune diseas; multiple sclerosis; human immunodeficiency virus; HIV; diabetes; rheumatoid arthritis; immune disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or molecules
                                               N-PSDB;
                                                                                                                                                                                                                                                Protein
                                                                                                                                                                                                                                                                                    Key
                                                                                                                                                                                                                                                                                                                                                                                                         Human CD4 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                    18-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB81502 standard;
                                                                                                                                   21-SEP-1999;
                                                                                                                                                            18-SEP-2000;
                                                                                                                                                                                     29-MAR-2001.
                                                                                                                                                                                                                                                                                                           Homo sapiens.
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                                                                                                                                                                                                                                                                       Peptide
                                                                                                          (AVID-)
                                                         2001-273470/28
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                                                                                                                                                                                                                                   26. .458
/label=
                                                                                                                                                                                                                                                         l. .25
/label=_Signal_peptide
                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein; 458
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99.5%;
                                                                                                                                                                                                                                   Human_CD4
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Pred. No. 4.8e-63;
0; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                            disease;
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Sequential screening of candidate compounds library for those which inhibit binding of low affinity receptor-ligand interaction having binding kinetics, using interfacial optical assay.

fast

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RESULT 62
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    used in an invention relating to a method for screening for compounds with the ability to inhibit a low affinity receptor-ligand interaction. The method uses an interfacial optical assay, such as surface plasmon resonance (SPR). The method is useful for screening candidate compounds for the ability to inhibit interaction between MHC/peptide complex and Tell receptor, and MHC/peptide complex and CDB or CD4 co-receptor. The compounds identified by the above methods which interfere with T cell receptor binding to a particular HLA type molecule are useful as immune inhibitors for treating carcinomas, autoimmune diseases such as multiple archive is the monodeficiency virus (HIV) infection, rheumatoid arthritis, Hashimoto's disease, insulin dependent diabetee, Good
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is human CD4. Human CD4 extracellular domains 1 an 2 were used in the construction of CD4 ollgomerisation fusion proteins. The fusion proteins contain an ollgomerisation domain that enables the proteins to bind to one another to form ollgomers. The ollgomers may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure;
             WPI; 2001-602565/68
                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                               Human; receptor; DC-SIGN; dendritic cell; T lymphocyte; HIV; gp120; C-type lectin; ICAM3; HIV entry; T cell; macrophage; HIV infection; CD4
                                                                                                                                                                                                                                                                                                                              Amino acid sequence of human
                                                                                                                                                                                                                                                                                                                                                                                                                            AAG79087 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 458
                                            Littman DR,
                                                                                                                         02-MAR-2000; 2000US-00517605
                                                                                                                                                        28-FEB-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TWTCTVLQNQKKVEFKIDIV 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180
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                                            Kwon D,
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NIJMEGEN.
                                                                                                                                                        2001WO-US006322
                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                           protein;
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99.5%;
                                          Van
                                            Kooyk Y,
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Pred. No. 4.8e-63;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                             CD4 protein.
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                                            Geijtenbeek
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An antibody for the treatment or prevention of HIV-infection comprises gp120 portion which binds to DC-SIGN or is exposed upon gp120 binding DC-SIGN due to concomitant conformational change.
                                                                                                                                         of a
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Disclosure; Page 115-116; 131pp; English.

Query Match Best Local S The specification describes an antibody which is specific for an antigenic fragment of gp120. This antigenic fragment binds to DC-SIGN or is exposed upon gp120 binding of DC-SIGN due to concomitant conformational change. DC-SIGN is a receptor that is specifically expressed on dendritic cells and facilitates infection of T lymphocytes with HIV. DC-SIGN is identical to a HIV-1 gp120-binding C-type lectin. I -SIGN binds ICAM-3 (which is expressed constitutively on T lymphocytes) with high affinity. The antibody of the invention inhibits the trans enhancement of HIV entry into a T cell or macrophage facilitated by dendritic cells. The antibody is useful to treat or prevent HIV infection. The present sequence represents a human CD4 protein Sequence 458 AA; 77.78; Score 1023; DB 4; Pred. No. 4.8e-63; .4 Length ဝူ g

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               TWTCTVLQNQKKVEFKIDIV 200
                                                   LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                               LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                           ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                          MNRGVP FRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
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TWTCTVLQNQKKVEFKIDIV 200
                                                                                                      ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
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밁 S

Local

Similarity

RESULT 63

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ADD25609 standard; protein;

(first entry)

neuroprotective; hinge region; immunoglobulin heavy chain; CH2 constant region; CH3 constant region; IgG1; antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation; Binding domain; immunoglobulin; fusion protein; cycostatto; antidarthritic; immunosuppressive; antidabetic; antityroid; immunoglobulin; fusion protein; cytostatic;

Binding domain-immunoglobulin fusion protein-associated protein #82.

malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma; rheumatoid arthritis; myasthenia gravis; Grave's disease; type I diabetes mellitus; multiple sclerosis; autoimmune disease.

US2003118592-A1

26-JUN-2003.

25-JUL-2002; 2002US-00207655

17-JAN-2001; 17-JAN-2002; 03-JUN-2002; 2001US-0367358P 2002US-00053530 2002US-0385691P

(GENE-) GENECRAFT

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Chinge region polypeptide; a mutated human IgG1 immunoglobulin (Chinge region polypeptide), a mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteline residues; where the mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (a) having a or more cysteline residues; where the first cysteline residues, where the first cysteline residues or more cysteline residues, where the mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteline residues, where the mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (contains of the mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteline residues; where the mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (contains of the mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (contains of the mutated human IgG1 immunoglobulin hinge region polypeptide contains on cysteline residues. The binding domain-immunoglobulin fusion protein is capable of at least one immunoglobulin hinge region polypeptide is capable of specifically binding to an construct comprising the polypucleotide (operably functionally the construct comprising the polypucleotide (operably inked to a promoter), construct comprising the binding domain-immunoglobulin fusion protein, a recombinant expression construct, producing the binding domain-immunoglobulin fusion protein, a recombinant expression construct, producing the binding domain-immunoglobulin fusion protein, a pharmaceutical composition comprising the binding domain-immunoglobulin fusion protein, a bost cell transformed or transfected with a recombinant expression construct, producing the binding domain-immunoglobulin fusion protein is useful for treating a subject construction or a B-cell disorder.

Construct the formal protein and construction or a B-cell disorder. The binding domain fusion protein is sequence is a binding domain fusio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New binding domain-immunoglobulin fusion protein, useful for treating a subject having or suspected of having a malignant condition or a B-cell disorder, e.g. melanoma, Grave's disease or autoimmune disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      number therefore
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181
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                                                TWTCTVLQNQKKVEFKIDIV 200
                                                                                                                                                                                                              LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     458 AA;
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                                                                                                                                                         LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         v/sequence.html?DocID=20030118592. The authors have not
equences in the printed specification by their SEQ ID
none of the sequences can be explicitly identified.
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Pred. No. 4.8e-63;
0; Mismatches 1
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Query Match Best Local Similarity

77.7**%;** 99.5**%**;

Score 1023; DB 7; Pred. No. 4.8e-63;

Length 458

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RESULT 64
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  comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a control that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal control to pain, a method for identifying an agent compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an enthod for identifying a compound which regulates the extraction, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypuptides or their antibodies. The polynucleotide given in the composition, a method for identifying a compound useful in treating polypoptides or their antibodies. The polynucleotide or the compound that composition comprising the one or more compound that sits activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction conjury (CCC) and spared nerve injury (SNI) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at fra winch in the part of the form willow at the composition of the printed control to the printed specification at the control control control to the printed co
Sequence 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic cons spared nerve injury; SNI; Chung.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or human polynucleotides or a polynucleotide which represents derivative or allelic variation of the nucleic acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention discloses a composition comprising two or more isolated or human polynucleotides or a polynucleotide which represents a fragme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page; 1017pp; English
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RESULT 65
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The invention relates to a composition for the treatment or prevention of human immunodeficiency virus-1 (HIV-1) infection. The composition comprises CD4+ cells that have been transduced with a vector that encode a chimeric CD4 molecule which is capable of being retained in the endoplasmic reticulum (ER). The invention also encompasses the use of a soluble protein factor produced by CD4+ cells that have been transduced with a vector encoding a chimeric CD4 protein; and the use of an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HIV-1 infection; human immunodeficiency virus-1; CD4+ cell; chimeric endoplasmic reticulum; ER retention; envelope protein gp160; T cell receptor CD3epsilon chain; C-terminal domain; CD4epsilon15;
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                                                                                                                                                                                                                                                                                                                                                                 fusion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LVEGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ILGNOGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                       HOSPITAL CORP.
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A
                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                 protein CD4Mmu.
                                                                                                                                                                               89CA-00588749
                                                                                                                                                                                                         89CA-00588749
                                                                                                                                                                                                                                                                                                                          r; CD4; gp120; immunoglobulin; Ig; SIV infection; medicament.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77.7%;
99.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                              474
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Pred. No. 5e-63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                                                        fusion protein;
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Example 1;

Page 47-53;

89pp; English

The invention provides a fusion gene encoding

D)

fusion protein that

fusion gene encoding immunoglobulin-CD4 fusion proteins, useful in treatment of HIV or simian immunodeficiency virus infections.

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RESULT 67
AAB19510
ID AAB19510
XX AAB19510
XX AAB19510
AX CD4-J
XX CD4-J
Y
XX CGEH
X
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Best Local (
                                                                                                                                             22-JAN-1988;
23-JAN-1989;
09-JUN-1992;
12-APR-1993;
04-FEB-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 comprises an extracellular CD4 DNA sequence or its fragment which binds to HIV gpl20 when fused to an immunoglobulin (Jg) chain and the DNA sequence of an Ig heavy or light chain, where the DNA sequence encoding the variable region has been replaced with the DNA sequence which encodes extracellular CD4 or its gpl20 binding fragment. The fusion protein is capable of being secreted. The fusion proteins are useful for treating HIV or SIV infections in animals, preferably humans. They are also useful for producing medicaments which can be used for treating HIV or SIV infections in humans. The present sequence represents the fusion protein CD4Mmu where the CD4 is linked to human IgG1 at the Mst2 site upstream of the CH1 region
WPI; 2000-586558/55
                                                                                                                                                                                                                                                                                                  07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                  12-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                 US6117656-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CD4; IgM; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CD4-IgM fusion protein CH4Pmu.
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                                                                                                 GEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ILGNQGSFLTKGPSKLNDRADSRRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
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                                                                                                    HOSPITAL CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                             88US-00147351.
89US-00299596.
92US-00896781.
93US-00057952.
94US-00191708.
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400. .4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CD4 Pmu;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .395
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99.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . 481
                                                                                                                                                                                                                                                                                                                                                                                                                                               "IgM heavy chain partial sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "CD4 extracellular region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fusion protein; immunoglobulin; HIV; SIV; gp120;
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Pred. No. 5e-63;
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The present sequence is that of fusion protein CD4Pmu comprising the extracellular portion of CD4, which binds to HIV gp120, linked at its C-terminus to the human IgM heavy chain. To obtain the fusion protein, DNA encoding CD4 was linked to IgM DNA at the Pst site upstream of the CH2 region (see AAA$0663). Fusion protein CD4Pmu and a nucleic acid encoding it are claimed. Also claimed are a vector comprising the nucleic acid, and a method of producing the fusion protein in secreted form using a transformed host cell. The fusion protein may further comprise a transformed host cell. The fusion protein may further comprise a therapeutic agent, radiolabel or NMR imaging agent. The fusion protein can be administered to an animal (including humans) for treatment of HIV or SIV infection, and can also be used in assays for HIV or SIV, imaging and tissue stains. IgM fusion proteins such as CD4Pmu provide complement—
                                                                                                                                                                                                                                                                                                                                                                                                                                                            \mathtt{CD4-immunoglobulin} fusion proteins, useful \mathtt{SIV}.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAA50662
                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Col 49-60; 39pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for targeting gp120
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181
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                                           MNRGVPFRHLLLVLQLALLPAATOGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                     | ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPL| IKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                    MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
TWTCTVLQNQKKVEFKIDIV
                      TWTCTVLQNQKKVEFKIDIV 200
                                                                                        ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                          60
                                                                  180
                                                                                                                                    60
                                                                                         120
                                                                                                             120
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Query Match Best Local Sim Matches 199;

Similarity

77.7%;

Conservative

0

Score 1023; DB 3; Pred. No. 5.1e-63; 0; Mismatches 1;

Length Indels

481; 0

Gaps

0

Sequence 481

A

mediated immunity

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RESULT 68
AAY51081
ID AAY51
22-JAN-1988;
23-JAN-1989;
09-JUN-1992;
12-APR-1993;
                                                                                                     Homo sapiens.
Synthetic.
                                                                                                                           Fusion protein; human; CD4; IgM; immunoglobulin; gp120; anti-human immunodeficiency virus; CD4Pmu.
                                                         04-FEB-1994;
                                                                                                                                                  Human fusion
                                                                                                                                                                 23-MAR-2000
                                                                        21-DEC-1999
                                                                                       US6004781-A.
                                                                                                                                                                                AAY51081;
                                                                                                                                                                                              AAY51081 standard;
      (GEHO ) GEN
       HOSPITAL CORP
                                                                                                                                                                 (first
                                                                                                                                                  protein
                    88US-00147351.
89US-00299596.
92US-00896781.
93US-00057952.
                                                         94US-00191708
                                                                                                                                                                                             protein;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention describes a novel nucleic acid (I) encoding a fusion protein comprising a DNA sequence encoding amino acids 1-173 of CD4 (II) and a DNA sequence encoding a mino acids 1-173 of cD4 (II) and a DNA sequence encoding a human immunoglobulin (Ig) heavy or light chain (III). The products pf the invention have anti-human immunodeficiency virus (HIV) activity and are capable of binding to gp120. The fusion protein is useful for treating human immunodeficiency virus (HIV) or similar immunodeficiency virus (SIV). This sequence represents the fusion protein CD4Pmu which is constructed from CD4 linke to human IgM upstream of the CH2 region
           WPI; 2000-063015/06
N-PSDB; AAZ48204.
                                                                                                                                                                                                                                                                                                         14-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seed
                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                               CD4-Ig fusion protein CD4Pmu
                                                                                                                                                                                                                                                                                                                                                         AAY59171 standard; protein; 481
                                                                                                                          20-JAN-1989;
                                                                                                                                                    14-SEP-1999
                                                                                                                                                                            CA1340741-C
                                                                                                                                                                                                                                          secreted protein;
                                                                                                                                                                                                                                                       HIV; extracellular;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 481 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Col 49-58;
                                                                                                   20-JAN-1989;
                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fusion protein useful for the treatment of human immunodeficiency virus
                                                                          (GEHO)
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DB; AAZ44064.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                          GEN
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                                                                                                                                                                                                                                                                                                                                                                                                                        TWTCTVLQNQKKVEFKIDIV
                                                                                                                                                                                                                                                                                                                                                                                                                                        TWTCTVLQNQKKVEFKIDIV 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                          HOSPITAL CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                   89CA-00588749
                                                                                                                           89CA-00588749
                                                                                                                                                                                                                                          r; CD4; gp120; immunoglobulin;
SIV infection; medicament.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1023; DI
Pred. No. 5.1e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                         200
                                                                                                                                                                                                                                                                                                                                                            ⋛
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; DB 3;
5.1e-63;
                                                                                                                                                                                                                                                      Įg;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                       fusion protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CD4 linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120
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FFX8X33333333333333XX
                                                                                                                                  New fusion gene encoding immunoglobulin-CD4 fusion proteins, useful the treatment of HIV or simian immunodeficiency virus infections.
                                                                                                                   54-60; 89pp; English
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The invention provides a fusion gene encoding a fusion protein that comprises an extracellular CD4 DNA sequence or its fragment which binds to HIV gp120 when fused to an immunoglobulin (1g) chain and the DNA sequence of an Ig heavy or light chain, where the DNA sequence encoding the variable region has been replaced with the DNA sequence which encodes extracellular CD4 or its gp120 binding fragment. The fusion protein is capable of being secreted. The fusion proteins are useful for treating HIV or SIV infections in animals, preferably humans. They are also useful for producing medicaments which can be sed for treating HIV or SIV infections. The present sequence represents the fusion protein in the fusion protein in animals. The present sequence represents the fusion protein could be seen to the fusion protein in the fusion p Sequence 481 CH2 region A A

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Best Local S
Matches 199
181
                        181
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                                                             121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                             199;
                                                                                             13
                                                                                                                     61
                                                                                                                                              _
                                                                                                                                                                                                      Similarity
                TWTCTVLQNQKKVEFKIDIV 200
                                                LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                             | ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                             MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                                          MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
TWTCTVLQNQKKVEFKIDIV
                                                                                              ILGNOGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                            Conservative
                                                                                                                                                                                                      77.7%;
99.5%;
                                                                                                                                                                                            0,
                                                                                                                                                                                            Score 1023; DB 3;
Pred. No. 5.1e-63;
0; Mismatches 1
200
                                                                                                                                                                                                                  DB 3;
                                                                                                                                                                                                                 Length
                                                                                                                                                                                             Indels
                                                                                                                                                                                                                     481;
                                                                                                                                                                                            0;
                                                                                                                                                                                            Gaps
                                                                                                                                              60
                                                                      180
                                                                                                120
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                                                180
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RESULT 70
AAB00158
ID AAB00
AAB00158
standard;
protein;
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AAB00158;

sCD4-SCFv(17b) HIV single chain antibody fusion protein. 08-FEB-2001 (first entry)

Fusion protein; HIV; human immunodeficiency virus; antibody; Fv, acquired immune deficiency syndrome; neutralisation; infection; gene therapy; CD4; gpl20; glycoprotein; resistance; vaccination; binding domain; single chain antibody; chimera; chimeric proteir

Human immunodeficiency virus

Synthetic.

WO200055207-A1

16-MAR-2000; 2000WO-US006946

16-MAR-1999; 99US-0124681P

) US NAT INST OF HEALTH

Berger ĘĄ, Del Castillo CM;

WPI; 2000-638183/61. N-PSDB; AAA54045.

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RESULT 71
AAR20152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CC (containing domains D1 and D2) fused to a single chain FV portion of CC antibody 17b via a linker. sCD4-SCFV(17b), its variant, analogue or mimetic is used for inactivating gp120 protein of HIV, and for centralising HIV. It is also used for blocking and preventing the binding CC of the viral or recombinant gp120 protein to soluble CD4 or lymphocyte CC therefore useful for treating HIV infection and also AIDS. It is are particularly useful in the prevention of infection during or immediately after HIV exposure (e.g., mother/infant transmission, post-exposure CC prophylaxis, and as a topical inhibitor) and for providing long term cresistance to HIV infections and AIDS. Gene therapy is used to secrete the bispecific protein at mucosal surfaces, such as the vaginal, rectal creative with neutralising antibody with high in vivo activity and no Fc mediated undesirable targetting properties. When the fusion protein is substantially derived from human proteins, it has minimal immunogenicity and toxicity in humans which is of great value in prevention of infection of during or immediately after HIV exposure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     binding to two sites of its target protein. The protein comprises a fibinding domain capable of binding to an inducing site on the target protein, a second binding domain capable of forming neutralising compwith an induced epitope of the target protein and a linker connecting binding domains. SCD4-SCFV(17b) comprises a soluble CD4 fragment
                                                                        acquired immune deficiency T helper lymphocytes.
                                                                                          Human immunodeficiency virus; HIV; gp 120; AIDS; ARC; glycoprotein; acquired immune deficiency syndrome; AIDS related complex;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel neutralizing bispecific fusion proteins effective in viral such as HIV neutralization, comprises two different binding domains, inducing-binding domain and induced-binding domain functionally linked by linker.
                                    Homo sapiens
                                                                                                                                                   Human CD4 sequence encoded by PATY.6.
                                                                                                                                                                                             25-MAR-2003
31-MAR-1992
                                                                                                                                                                                                                                                                                        AAR20152 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 507 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sCD4-SCFv(17b) is a neutralising bispecific fusion protein capable of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 39; Page 46-47; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
                                                                                                                                                                                                                                                                                                                                                                                         181
                                                                                                                                                                                                                                                                                                                                                                                                                            181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      199;
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                                                                                                                                                                                                                                                                                                                                                                                     TWTCTVLQNQKKVEFKIDIV 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
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                                                                                                                                                                                           (revised)
(first en
Location/Qualifiers
                                                                                                                                                                                                                                                                                          protein; 519
                                                                                                                                                                                           entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             its target protein. The protein comprises a f binding to an inducing site on the target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1023; DB 3;
Pred. No. 5.4e-63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
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RESULT 72
AAY51082
ID AAY51
XX Fusic
XW Fusic
XW AAT1XX AAY51
XX AAY51
XX

Human fusion

(first entry)
protein CD4Bgammal.

AAY51082; 23-MAR-2000

Homo sapiens. Synthetic. US6004781-A. AAY51082 standard;

protein;

Fusion protein; human; CD4; IgG1; immunoglobulin; gp120; anti-human immunodeficiency virus; CD4Bgamma1.

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                                                                                                                                                                                                                   Matches 199;
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Best Local
                                                                                                                                                                                                                                                                                                             The sequence was deduced from the DNA sequence of subclone PATY.6, conty DNA coding for the full-length human CD4. The clone was constructed from plasmids pBG178A and pBG378 (both in USB02940). The DNA can be used to express recombinant CD4 and analogues for use in diagnosis and treatment of diseases caused by infective agents whose primary targets are T4+ lymphocytes. See also AAR20148-R20155 and AAR21078. (Updated on 25-MAR-
                                                                                                                                                                                                                                                                                                                                                                                                                                 New immuno-therapeutic human CD4 variants and derivs. - production to HIV gp.120, useful in treating, preventing AIDS, ARC and HIV infections.
                                                                                                                                                                                                                                                                     Sequence 519
                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 28; 179pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAQ20327.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1992-007200/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fisher RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-MAY-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-DEC-1991.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BIOJ ) BIOGEN INC
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 242
                                                                              121
                                                                                                          122
                         181
                                                     182
                                                                                                                                    61
                                                                                                                                                            62 MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 121
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                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                correct PA field.)
                                                                    LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                         ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                             MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                         ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
TWTCTVLQNQKKVEFKIDIV
                          TWTCTVLQNQKKVEFKIDIV 200
                                                     LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hession
                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90US-00529186
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/label= signal_sequence
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                                                                                                                                                                                                                              77.78;
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                                                                                                                                                                                                                              Score 1023; DB 2;
Pred. No. 5.5e-63;
 261
                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                              treating, preventing and
                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               elicit AB
                                                                                                                                                                                                                 0;
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                                                                                                                                                                                                                 Gaps
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RESULT 73
AAY59172
ID AAY59
XX AAY59
AC AAY59
XX 14-MA
AC AAY59
XX 14-MA
AC AAY59
XX 14-MA
AC AAY59
XX 14-MA
AC AAY59
XX 50
AC AAY59
XX 60
AC AAY59
AAY50
AA
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Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 199;
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23-JAN-1989;
09-JUN-1992;
12-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention describes a novel nucleic acid (I) encoding a fusion protein comprising a DNA sequence encoding amino acids 1-173 of CD4 (II) and a DNA sequence encoding a minon acids 1-18 of chain (III). The products pf the invention have anti-human immunodeficiency virus (HIV) activity and are capable of binding to gp120. The fusion protein is useful for treating human immunodeficiency virus (HIV) or similan immunodeficiency virus (SIV). This sequence represents the fusion protein CD4Egammal which is constructed from CD4 linked to human IgG1 upstream of the hinge region
                           14-SEP-1999
                                                                                                                                                                                                           HIV; extracellular; CD4; gp120; immunoglobulin; Ig; fusion protein; secreted protein; SIV infection; medicament.
                                                                                                                                                                                                                                                                                                                                            14-MAR-2000
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                                                                            CA1340741-C
                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY59172 standard; protein; 616
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fusion protein useful for the treatment
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                                                                                                                              sapiens
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DB; AAZ44065.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TWTCTVLQNQKKVEFKIDIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
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                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                        protein CD4Bgammal.
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89US-00299596.
92US-00896781.
93US-00057952.
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99.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   200
                                                                                                                                                                                                                                                                                                                                                                                                                                                    B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of human immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 616;
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ARESULT 74
AAP33009
ID AAP8
XX AAP8
XX AAP8
XX CAAP9
XX CAAP6
XX CAAP6
XX CAAP6
XX CAAP6
XX Fuel
KW diag
XX Homc
XX Homc
XX Homc
XX Homc
XX Hom
XX Ho
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Best Local Similarity
Matches 199; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention provides a fusion gene encoding a fusion protein that comprises an extracellular CD4 DNA sequence or its fragment which binds to HIV gp120 when fused to an immunoglobulin (1g) chain and the DNA sequence of an Ig heavy or light chain, where the DNA sequence encoding the variable region has been replaced with the DNA sequence which encodes extracellular CD4 or its gp120 binding fragment. The fusion protein is capable of being secreted. The fusion proteins are useful for treating HIV or SIV infections in animals, preferably humans. They are also useful for producing medicaments which can be used for treating HIV or SIV infections. The present sequence represents the fusion protein CD4Bgammal where the CD4 is linked to human IgG1 at the Banl site
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                                                                                                                                                                                                    Fusion protein;
diagnosis; CD4;
                                                                                                                                                                                                                                                                                                                                                                                   25-MAR-2003
02-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 616
                                                                                                                                                                                                                                                                                                                            Genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAP93009;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAP93009 standard; protein;
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N-PSDB; AAZ48205.
                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                             upstream
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          downstream from the hinge region
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                                                                                                                                                                                                                                                                                       construct which encodes CD4 linked to human IgG1 at the Esp m of the hinge region (fusion protein CD4E-gamma-1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
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                                                                                                                                                                                                                                                                                                                                                                             (revised)
(first entry)
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                                                                                                                                                                                                    immunoglobulin-like molecule; HIV; SIV; therapy;
gpl20; binding fragment; glycoprotein; variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77.7%;
99.5%;
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Pred. No. 6.7e-63;
0; Mismatches 1
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0

180 180 120 120

26-JUL-1989 EP325262-A.

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RESULT 75
AAB19508
ID AAB19
XX AAB19
XX AAB19
XX O9-JA
XX CD4-I
XX CD4;
XW CD4;
XW GP120
XX GP120
XX Prote
FT Prote
FT Prote
FT Prote
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The fusion protein genes of the invention pref. comprise cDNA sequences which encode CD4 or a fragment which binds gpl20 ligated to an expression plasmid which encodes an antibody in which the variable region of the gene has been deleted (see W087-02671). The CD4 portion of the fusion protein may comprise the complete CD4 sequence, the 370 AA extracellular region and the membrane spanning domain, or the extracellular region. The IJ heavy chain is pref. from IJM, IJG11 or IJG3. The following are specifically claimed: fusion proteins CD4H-gamma-1, CD4Hmu, CD4E-gamma1, and CD4Hmu (NO.6760B), pCD4P-gamma (NO.6760B) and pCD4E-gamma-1 (NO.6760B). The plasmid containing (pCD4E-gamma-1) has been deposited in E. coli (MC1061/PJ) at the ATCC under accession number 67610. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                             CD4; IgG1; humar gp120; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1989-214472/30.
N-PSDB; AAN90357.
                             Protein
                                                          Protein
                                                                                                  Homo sapiens
                                                                                                                                                                                                    09-JAN-2001
                                                                                                                                                                                                                                                           AAB19508 standard; protein; 631 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 631 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunoglobulin-CD4 fusion proteins - used for infections or detecting HIV or SIV in sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-JAN-1988;
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                                                                                                                                                                        fusion protein CH4Egammal.
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                                                                                                                             human; CD4Egamma1; fusion rapy; diagnosis.
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                             400.
                                                                    Location/Qualifiers
                /note= "IgG1 heavy chain"
                                         note= "CD4 extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77.7%;
                            .631
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Pred. No. 6.9e-63;
0; Mismatches 1;
                                                                                                                                            protein; immunoglobulin;
                                         region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                treating
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                                                                                                                                             HIV;
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RESULT 76
AAY51079
ID AAY51
XX
AC AAY51
XX
DT 23-MA
XX
DE Human
XX
KW Fusic
KW anti-

AAY51079

standard;

protein; 631 AA

180 180 120 120

0

23-MAR-2000

(first

entry)

Fusion protein; human; CD4; IgG1; immunoglobulin; gp120; anti-human immunodeficiency virus; CD4Egamma1.

Human fusion protein CD4Egammal.

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Best Local S
Matches 199
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23-JAN-1989;
09-JUN-1992;
                                                                                                                                                                                                                                                                                                                                      The present sequence is that of fusion protein CD4Bgammal comprising the extracellular portion of CD4, which binds to HIV gp120, linked at its C-terminus to the human IgG1 heavy chain. To obtain the fusion protein, DNA encoding CD4 was linked to IgG1 DNA at the Esp site upstream of the hinge region (see AAA50661). Fusion protein CD4Bgammal and a nucleic acid encoding it are claimed. Also claimed are a vector comprising the nucleic acid, and a method of producing the fusion protein in secreted form using a transformed host cell. The fusion protein may further comprise a therapeutic agent, radiolabel or NMR imaging agent. The fusion protein can be administered to an animal (including humans) for treatment of HIV or SIV infection, and can also be used in assays for HIV or SIV, imaging and tissue stains. IgG1 fusion proteins such as CD4Bgammal provide both complement-mediated and cell-mediated immunity
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N-PSDB; AAA50661.
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04-FEB-1994;
                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CD4-immunoglobulin fusion proteins, useful for targeting gp120 of HIV
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181
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                                                          LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                           LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                          ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                    MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
TWTCTVLONOKKVEFKIDIV 200
                TWTCTVLQNQKKVEFKIDIV 200
                                                                                                                         ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
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89US-00299596.
92US-00896781.
93US-00057952.
94US-00191708.
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                                                                                                                                                                                                                                                            77.7%;
99.5%;
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                                                                                                                                                                                                                                               Score 1023; DB 3;
Pred. No. 6.9e-63;
0; Mismatches 1
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AAY59169
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Best Local Similarity
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23-JAN-1989;
09-JUN-1992;
12-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes a novel nucleic acid (I) encoding a fusion protein comprising a DNA sequence encoding amino acids 1-173 of CD4 (II) and a DNA sequence encoding amino acids 1-18 heavy or light chain (III). The products pf the invention have anti-human immunodeficiency virus (HIV) activity and are capable of binding to gp120. The fusion protein is useful for treating human immunodeficiency virus (HIV) or simian immunodeficiency virus (SIV). This sequence represents the fusion protein CD4Egammal which is constructed from CD4 linked to human IgG1 upstream of the hinge region
                      HIV; extracellular; CD4; gp120; immunoglobulin; secreted protein; SIV infection; medicament.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                     14-MAR-2000
                                                                                                                                      AAY59169 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fusion protein useful
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N-PSDB; AAZ44062.
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Synthetic.
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                                                                                                                                                                                                                                                                    LVFGLTANSDTHLLQGQSLTLTLESSPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                                                   TWTCTVLQNQKKVEFKIDIV
                                                                                                                                                                                                                                                                                                     ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                                                                                                                      ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
                                                                                                                                                                                                                                                                                                                                                       MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                                                                                                                                                                                                                                                       MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
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                                                                                    (first entry)
                                                           protein CD4Egamma1.
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89US-00299596.
92US-00896781.
93US-00057952.
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Pred. No. 6.9e-63;
0; Mismatches 1;
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                                     fusion
                                  protein;
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RESULT 78
AAP93008
ID AAP9
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AC AAP9
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DT 25-M
DT 02-N
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DE Gene
DE Site
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Best Local
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             Fusion protein;
diagnosis; CD4;
                                                    Genetic construct which encodes site upstream of the CH1 region
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N-PSDB; AAZ48202.
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02-NOV-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fusion gene encoding immunoglobulin-CD4 fusion proteins, use treatment of HIV or simian immunodeficiency virus infections
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(first entry)
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           immunoglobulin-like molecule; HIV; SIV; therapy;
gpl20; binding fragment; glycoprotein; variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77.7%;
99.5%;
                                                                                                                                                                     729
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Pred. No. 6.9e-63;
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                                                    CD4 linked to human IgG1 at the (fusion protein CD4H-gamma-1).
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RESULT 79
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CD4-I
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                                                       CD4; IgG1; human; CD4Hgamma1; fusion protein; immunoglobulin; HIV;
                                                                                                               09-JAN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunoglobulin-CD4 fusion proteins - used for infections or detecting HIV or SIV in sample.
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                                       therapy;
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                                                                                   fusion protein CH4Hgammal.
                                                                                                                                                                       standard;
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                                       diagnosis.
                                                                                                                                                                    protein; 729
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Pred. No. 8.1e-63;
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RESULT 80
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AC AAY51
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AAY51078 standard;

protein; 729

AAY51078;

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09-JUN-1992;
12-APR-1993;
04-FEB-1994;
                                                                                                                                                                                                                                                                          The present sequence is that of fusion protein CD4Hgammal comprising the extracellular portion of CD4, which binds to HIV gpl20, linked at its C-terminus to the human IgG1 heavy chain. To obtain the fusion protein, DNA encoding CD4 was linked to IgG1 DNA at the Hind3 site upstream of the CH1 region (see AAA50660). Fusion protein CD4Hgammal and a nucleic acid encoding it are claimed. Also claimed are a vector comprising the nucleic acid, and a method of producing the fusion protein in secreted form using a transformed host cell. The fusion protein may further comprise a therapeutic agent, radiolabel or NMR imaging agent. The fusion protein can be administered to an animal (including humans) for treatment of HIV or SIV infection, and can also be used in assays for HIV or SIV, imaging and tissue stains. IgG1 fusion proteins such as CD4Hgammal provide both complement-mediated and cell-mediated immunity
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DB; AAA50660.
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                                                                                                                                                                                                                Similarity
                                                LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                               LVFGLTANSDTHLLQGQSLTLTLESPEGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
TWICTVLONOKKVEFKIDIV
               TWTCTVLQNQKKVEFKIDIV
                                                                                                 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
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89US-00299596.

92US-00896781.

93US-00057952.

94US-00191708.
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400. .729
/note= "IGG1 heavy chain"
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                                                                                                                                                                                                               77.7%;
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                                                                                                                                                                                                               Score 1023; DB 3;
Pred. No. 8.1e-63;
200
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                                                                                                                                                                                                                              DB 3;
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                                                                                                                                                                                                                            Length 729;
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RESULT 81
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AC AAY59
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Best Local
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09-JUN-1992;
12-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes a novel nucleic acid (I) encoding a fusion protein comprising a DNA sequence encoding amino acids 1-173 of CD4 (II) and a DNA sequence encoding a human immunoglobulin (Ig) heavy or light chain (III). The products pf the invention have anti-human immunodeficiency virus (HIV) activity and are capable of binding to gp120. The fusion protein is useful for treating human immunodeficiency virus (HIV) or simian immunodeficiency virus (SIV). This sequence represents the fusion protein CD4H-1 which is constructed from CD4 linked to human IgG1 upstream of the CH1 region
              14-MAR-2000
                                       AAY59168;
                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-085792/07
                                                             AAY59168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Col 15-30; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fusion protein useful for the treatment of human immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-FEB-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-DEC-1999
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                                                                                                                                                                                                                                                                                         1 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
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                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                           TWTCTVLQNQKKVEFKIDIV 200
                                                                                                                                                                                                                                            ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
                                                                                                                                                                                                                                                                                                                                                                                729
                                                             standard;
                                                                                                                            TWTCTVLQNQKKVEFKIDIV 200
                                                                                                                                                                            LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                                  LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180
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                                                                                                                                                                                                                                                                           MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tein; human; CD4; IgG1; immunoglobulin;
immunodeficiency virus; CD4H-1.
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             (first entry)
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92US-00896781.
93US-00057952.
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                                                             protein;
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99.5%;
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                                                                                                                                                                                                                                                                                                                                                      DB 3;
                                                                                                                                                                                                                                                                                                                                                     Length 729;
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RESULT 82 AAR26530

AAR26530

standard;

protein;

SABAAAA

AAR26530

25-MAR-2003 28-JAN-1993

(revised)
(first entry)

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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                               The invention provides a fusion gene encoding a fusion protein that comprises an extracellular CD4 DNA sequence or its fragment which binds to HIV gp120 when fused to an immunoglobulin (1g) chain and the DNA sequence of an Ig heavy or light chain, where the DNA sequence encoding the variable region has been replaced with the DNA sequence which encodes extracellular CD4 or its gp120 binding fragment. The fusion protein is capable of being secreted. The fusion proteins are useful for treating HIV or SIV infections in animals, preferably humans. They are also useful for producing medicaments which can be add for treating HIV or SIV infections in humans. The present sequence represents the fusion protein CD4Hgammal where the CD4 is linked to human IgG1 at the Hind3 site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-063015/06.
N-PSDB; AAZ48201.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HIV; extracellular; CD4; gp120; immunoglobulin; Ig; fusion protein; secreted protein; SIV infection; medicament.
                                                                                                                                                                                                                                                                                                        Sequence 729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New fusion gene encoding immunoglobulin-CD4 fusion proteins, useful the treatment of HIV or simian immunodeficiency virus infections.
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181
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            TWTCTVLQNQKKVEFKIDIV 200
                                                                                                                                    ILGNQGSFLTKGPSKLNDRADSRRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                               MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                                                                                MNRGVPFRHLLLVLQLALLPAATQCNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                                                                                                                                                                                                                    of the CH1 region
                                                         LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                     ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
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99.5%;
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Pred. No. 8.1e-63;
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                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                               Example; Fig 3; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                      CD4-gamma 1 chimeric heavy chain homo-dimer and its expression vector for preventing and treating HIV infection useful as a diagnostic agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-FEB-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-FEB-1992;
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les 204; Conserv
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                                                            VFGLTANSDTHLLQCQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGT
                                                                                                               LGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLL
                                                                                                                                               NRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKI
                                                                                                                                                              NRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diagnostic
WTCTVLQNQKKVEFKIDIVVLAFEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKP
                  WTCTVLQNQKKVEFKIDIV------PRASALPAPPTGSALPDPQTASALPDP
                                                                                               LGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLL
                                               VFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGT
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/note= "1. .25:
205. .219
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/label= CH2
330. .436
/label= CH3
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agent;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INC.
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                                                                                                                                                                                               Score 1021.5; DB 2;
Pred. No. 5.8e-63;
1; Mismatches 21;
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                                                                                                                                                                                                Indels
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235
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RESULT 83 ADE65841

25-MAR-2003

AAP93012;

AAP93012 standard;

protein; 614

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RESULT 84
AAP93012
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AC AAP93
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Matches 198;
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                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    preparing a protein array useful for screening drug targets comprises depositing an array of a first protein on substrate, and applying a second protein comprising an amino acid sequence that binds to a doma: of the first protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; CD4 receptor; protein array; PDZ do
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 25; 60pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-MAR-2002; 2002US-00092138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-MAR-2002; 2002US-00092138.
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                                                                                                                                                                                                                                                           1LGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
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                                                                                                                             TWTCTVLQNQKKVEFKIDIV
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domain; drug target screening.
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99.0%;
                                                                                                                                                                                                                                                                                                                                                       Score 1021; DB 7;
Pred. No. 6.7e-63;
1; Mismatches 1
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03-AUG-1992

(first entry)

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RESULT 8:
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ID AAP:
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AC AAP:
XC AAP:
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DT 25-1
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Matches 198; Conserv
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              25-MAR-2003
03-AUG-1992
                                                       AAP93011;
                                                                                 AAP93011
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 614
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genetic construct which encodes CD4 linked to human IgG1 at the Banl downstream from the hinge region (fusion protein CD4Blambdal).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunoglobulin-CD4 fusion proteins - used for treating infections or detecting HIV or SIV in sample.
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                                                                                                                                                                        TWTCTVLQNQKKVEFKIDIV 200
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                                                                                 standard;
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gp120; binding fragment; glycoprotein; variable
                                                                                protein;
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99.0%;
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Pred. No. 1.5e-62;
D; Mismatches 2;
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RESULT 86
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                                                  07-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1989-214472/30
N-PSDB; AAN90359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genetic construct which encodes CD4 linked to human upstream of the CH2 region (fusion protein CD4Pmu).
                       The soluble extracellular domain of the T4 glycoprotein.
                                                                                                    AAB07768
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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infections or detecting HIV or SIV in sample.
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diagnosis; CD4;
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                                                                                                  standard; protein;
                                                                                                                                                                                     TWTCTVLQNQKKVEFKIDIV
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                                                                                                                                                                                                                                     LVEGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
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                                                                                                                                                                      TWTCTVLONOKKVEFKIDIV
                                                                                                                                                                                                                                                                           ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEAQKEEVQL
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gp120; binding fragment; glycoprotein;
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99.0%;
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Pred. No. 1.8e-62;
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Human; T4 glycoprotein; human immunodeficiency virus; HIV

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RESULT 87
AARO6373
ID AARO6
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AC AARO6
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AC AARO6
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DT 31-OC
DT 20-DE
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11-JUN-1991;
06-JUL-1992;
12-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents an aqueous-soluble polypeptide comprising a portion of a human T4 glycoprotein. The portion specifically forms a complex with a human immunodeficiency virus (HIV) envelope glycoprotein. The DNA is useful for producing the soluble surface T4 glycoprotein. The soluble surface T4 glycoprotein is useful as a therapeutic agent, i.e. as prophylaxis for treating a subject infected with an HIV virus. Thus, the soluble T4 glycoprotein is useful for treating human AIDS. The soluble T4 glycoprotein is useful for treating human AIDS. The soluble T4 glycoprotein is also useful in diagnostic or screening assays, e.g. for screening inhibitors of virus binding, or for detecting and quantitating T4, T4+ cells and antibodies to T4, which are of diagnostic value for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated nucleic acid encoding a soluble surface T4 glycoprotein that for treating a subject infected with
              31-OCT-2002
20-DEC-1990
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N-PSDB; AAA59351.
                                                      AAR06373;
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drome virus.
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197; Conserv
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                                                                                                                                                                                                                      LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                                                                                         | ILGNQGSSLTKGPSKLNDRADSRRSLWDQGNFPLIIRNLKIEDSDTYICEVEDQKEEVQL
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                                                                                standard;
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              (revised)
(first entry)
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91US-00713564.
92US-00909021.
94US-00354452.
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                                                                              protein;
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Pred. No. 2.4e-62;
1; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human T cell surface protein and it encodes, useful as prophylaxis human acquired immune deficiency
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Matches 198;
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                                                                                                                                                                                                                                      Soluble T4 can be produced by truncating the CDS to remove the transmembrane and cytoplasmic domains. The soluble forms may be modified to increase their immunogenicity by addition of an adjuvant such as incomplete Freund's adjuvant. The T4 interferes with HIV/T4 interaction and elicite anti-soluble T4 antibody production. Soluble T4 proteins include the following polypeptide fragments: amino acids 1-385, 24-385, Met-24-385, 24-397, 1-400 and Met-24-400. See also AAQOS608. (Updated on 31-OCT-2002 to add missing OS field.)
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                                                                                                                                                                                                                                                                                                                                                                      Treating or preventing AIDS, ARC or HIV infection - by administering immunologically effective amt. of soluble T4 protein.
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N-PSDB; AAQ05607.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-JAN-1989;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9008198-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                               Letvin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HARD ) HARVARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-JAN-1989;
 181
                        121
                                              121
                                                                       61
                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                                               NA
                                                                                                                                 1 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                                                               Similarity
                                    LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
TWTCTVLQNQKKVEFKIDIV 200
                                                                     ILGNQGSFLTKGPSKLNDRADSRRSLRDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                   ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                     MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     γģ
                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     plasmid p170-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89US-00300096.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89US-00300096.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COLLEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            soluble T4 protein; AIDS; ARC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= transmembran
/note= "hydrophobic"
419. 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      398.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= extracellular
/note= "homology to V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "glycosylated
398. .418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "homology to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         abel= extracellular
                                                                                                                                                                             76.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            el= hydrophobic/secretory signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "very hydrophilic"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transmembrane sequence
                                                                                                                                                                   0
                                                                                                                                                                 Score 1009; DB 2;
Pred. No. 4.5e-62;
0; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J-regions'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    V-regions"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                region"
                                                                                                                                                                                          Length 458;
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181

TWTCTVLQNQKKVEFKIDIV

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RESULT 88
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                                                                                                                Matches
                                                                                                                           Query Match
Best Local
                                                                                                                                                                                        The polypeptides encoded are useful in immunotherapeutic, prophylactic and diagnostic compans. They can be used to purify HIV from a sample. The soluble T4 protein-based compans. are useful in treating immunodeficient patients suffering from diseases caused by agents whose primary targets are T4+ lymphocytes. They can be used for preventing, treating or detecting AIDS, ARC and HIV infection. (Updated on 25-MAR-2003 to correct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HIV;
                                                                                                                                                                                                                                                                                             DNA sequences coding for soluble T4-like polypeptide(s) - used in immuno:therapeutic and immunosuppressive compsns. and for preventing treating or detecting AIDS.
                                                                                                                                                                                                                                                                                                                                                                              Fisher
                                                                                                                                                                                                                                                                                                                                                                                                                                    04-SEP-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-MAR-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence encoded by T4 lymphocyte cDNA obtained from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAP94703 standard; protein;
                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                          Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                           07-JAN-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-SEP-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo
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22-MAR-1991
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                                                                                                                                                                                                                                                                                                                                                                                                    (BIOJ )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO8901940-A
                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                       1989-085519/11.
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  121
                       127
                                             61
                                                                   67
                                                                                                                198;
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                                                                                                                                                                                                                                                                                                                                                                                                    BIOGEN INC
                                                                                                                           Similarity
                                                                               MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
                                                                                                                                                           524
LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                     ILGNQGSFLTKGPSKLNDRADSRRSLRDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                   ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
                                                                  MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 126
                                                                                                                                                                                                                                                                        Fig 3; 207pp;
                                                                                                              76.6%; llarity 99.0%; Conservative
                                                                                                                                                                                                                                                                                                                                                                              Gilbert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T4;
                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (revised)
(first en
                                                                                                                                                                                                                                                                                                                                                                                                                         87US-00094322
88US-00141649
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note= "AA DESIGNATED NUMBER 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunotherapeutic; prophylactic; diagnostic; AIDS; ARC
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                                                                                                                                                                                                                                                                                                                                                                              Sato
                                                                                                                                                                                                                                                                         English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            524
                                                                                                              Score 1009; DB 1;
Pred. No. 5.3e-62;
D; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                            Maraganore JM;
                                                                                                                                    Length 524;
                                                                                                               Indels
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460

ILGNQGSFLTKGPSKLNDRADSRRSLRDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL

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RESULT 89
AAR07640
ID AAR07
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                                                                                       Query Match
Best Local Similarity
Matches 198; Conserv
                                                                                                                                                                  Entire sequence from T4-encoding plasmid p170-2. It is almost identical to the sequence published by Maddon et al. (1985) with the exception of three codon changes. At T4 amino acid residue 3, (posn. 403 of entire sequence) Lys is encoded in stead of Asn. At posn. 64, (posn. 464) Arg replaces Txp and at posn. 23, (posn. 631) Ser replaces Phe. Soluble T4 can be produced by truncating the CDS to remove the transmembrane and cytoplasmic domains. The soluble forms may be modified to increase their immunogenicity by addition of an adjuvant such as incomplete Freund's adjuvant. The T4 interferes with HIV/T4 interaction and elicits antisoluble T4 antibody production. See also AAQ05608. (Updated on 31-OCT-2002 to add missing OS field.)
                                                                                                                                                                                                                                                                                                                                                            Treating or preventing AIDS, ARC or HIV infection - by administering an immunologically effective amt. of soluble T4 protein.
                                                                                                                                            Sequence 2458 AA;
                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 1; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAQ05607.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    plasmid p170-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-OCT-2002
20-DEC-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR07640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR07640 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1990-254040/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Letvin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-JAN-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-JAN-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-JUL-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 řey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Deduced protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HARD ) HARVARD COLLEGE
                                      400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181
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            5
ILGNQGSFLTKGPSKLNDRADSRRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                    MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TWTCTVLQNQKKVEFKIDIV 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TWTCTVLQNQKKVEFKIDIV 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LVPGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                      MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89US-00300096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   soluble T4 protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= T4 surface glycoprotein
                                                                                                   76.6%;
99.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             p170-2 comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2458
                                                                                        0
                                                                                        Score 1009; DB 2;
Pred. No. 2.9e-61;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AIDS; ARC; HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T4.
                                                                                          2
                                                                                                                   Length
                                                                                          Indels
                                                                                                                   2458;
                                                                                          0
            120
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31-OCT-2002
29-MAY-1990
                  The sequence differs from that determined by PJ Madden et al., [Cell, 42 pp. 93-104 (1985)] in three places due to three nucleotide substitutions. The Asp reported at position 3 by Madden et al. was the result of a sequencing error [DR Littman et al. Cell, 55, p.541 (1988)]. X = stop codon. The sequence was deduced from the cDNA insert of p170-2. Soluble T4 constructs may be produced by truncating this sequence to give fragments from position 400 to 799, removing the transmembrane and intracytoplasmic domains whilst retaining the extracellular region responsible for HIV binding. The sol. T4 is combined with an anti-viral agent such as AZT. See also AAQ03006. (Updated on 31-OCT-2002 to add missing OS field.) (Updated on 25-MAR-2003 to correct PA field.)
  Sequence
                                                                                                                                                        Disclosure; Fig 1; 100pp; English.
                                                                                                                                                                                          Combinations of soluble T4 protein and anti-retro:viral agent synergistic activity in treatment and prevention of AIDS, arc
                                                                                                                                                                                                                            N-PSDB; AAQ03005
                                                                                                                                                                                                                                        WPI; 1990-007302/01.
                                                                                                                                                                                                                                                              Fisher
                                                                                                                                                                                                                                                                                                                                         20-APR-1989;
                                                                                                                                                                                                                                                                                                                                                   10-JUN-1988;
                                                                                                                                                                                                                                                                                                                                                                         08-JUN-1989;
                                                                                                                                                                                                                                                                                                                                                                                               14-DEC-1989
                                                                                                                                                                                                                                                                                                                                                                                                                    WO8911860-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Soluble T4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Full length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR04031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR04031 standard;
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COIE)
COIE)
COIE)
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                                                                                                                                                                                                                                                            RA,
                                                                                                                                                                                                                                                                                 ) BIOGEN NV INC.
) GEN HOSPITAL CORP.
) BIOGEN INC.
  2458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TWICTVLONOKKVEFKIDIV 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TWTCTVLQNQKKVEFKIDIV 200
                                                                                                                                                                                                                                                            Schooley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      p170-2; anti-retroviral agent; AIDS; ARC; HIV; AZT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T4 encoded by plasmid p170-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (revised)
(revised)
(first entry)
  ß,
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89US-00341080.
                                                                                                                                                                                                                                                                                                                                                                         89WO-US002453
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Asp of Madden et al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Phe of Madden
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note= "Trp of Madden
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein; 2458
                                                                                                                                                                                                                                                            RT,
                                                                                                                                                                                                                                                            Hirsch MS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ā
                                                                                                                                                                                                                                                            Johnson
                                                                                                                                                                                                                                                                                                                                                                                                                                         et al
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                                                                                                                                                                                                                                                                                                                                                                                                                                         replaced by Ser"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     replaced
                                                                                                                                                                                                                                                            ٧A,
                                                                                                                                                                                                                                                             Walker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                by Lys"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     λq
                                                                                                                                                                                                                                                             BD;
                                                                                                                                                                                          - having
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Query Match

76 . 6%;

Score 1009;

DB

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Length 2458;

The T4 protein encoded by p170.2 is almost identical to that reported by P.J. Maddon et al [Cell, 42, pp 93-104 (1985)]. The Maddon sequence was revised in 1988 to correct a DNA sequencing error at AA 3 (corrected from Asp to Lye; see M12807 in GenBank). The DNA may be truncated (to remove transmembrane and intracellular regions) and/or modified by SDM, pref. so the prod. extends from AAs 3-183 of the mature protein. This DNA can then

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RESULT 91
AAR04910
ID AAR0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 99.0 Matches 198; Conservative
                                                                                   New immunotoxin contg. soluble T4 protein components and toxin - esp. Pseudomonas endotoxin A, for treating or controlling AIDS and related conditions, and new DNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                       T4 protein; angiogenin;
                                                                                                                                                                                                                                                                                                                                                                                                                                       31-OCT-2002
02-OCT-1990
                                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                  Key
                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                   T4 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR04910;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR04910 standard;
                                                                 Disclosure; Page ?; -pp;
                                                                                                                                                     Meade HM,
                                                                                                                                                                                            18-OCT-1988;
                                                                                                                                                                                                                18-OCT-1988;
                                                                                                                                                                                                                                   03-MAY-1990
                                                                                                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                                                                                                      Protein
                                                                                                                                                                                                                                                     WO9004414-A
                                                                                                                                                                                                                                                                                                                                        Peptide
                                                                                                                                                                        (BIOJ ) BIOGEN INC
                                                                                                                          1990-163876/21.
DB; AAQ04555.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    580
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(first ent
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                                                                                                                                                                                                                                                                      /label= T4 protein
replace(87,W)
/note= "differs from Madden
replace(254,F)
/note= "differs from Madden
                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                              /label= signal peptide
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0; Mismatches 2;
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RESULT 92
AAR11285
ID AAR11
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Best Local S
Matches 197
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09-JAN-2003
29-APR-1991
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                          New non-human primate and human CD4 or gp120 molecules - used to treat HIV or SIV and immunoglobulin and gp120 binding molecules from new fus proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
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DB; AAQ10887.
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(revised)
(first entry)
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98.5%;
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Pred. No. le-61;
l; Mismatches
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RESULT 93
AAR20151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Key
Peptide
                                                                                      New immuno-therapeutic human CD4 production to HIV gp.120, useful AIDS, ARC and HIV infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human immunodeficiency virus; HIV; gp 120; AIDS; ARC; glycoprotein; acquired immune deficiency syndrome; AIDS related complex;
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31-MAR-1992
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                                                                                                                                                                               N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chimpanzee
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                                          Claim 15; Fig 21; 179pp; English.
                                                                                                                                                                                                      WPI; 1992-007200/01.
                                                                                                                                                                                                                                                   Fisher
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                                                                                                                                                                                                                                                                                                                                         25-MAY-1990;
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/label= signal_sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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98.0%;
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Pred. No. 1.4e-61;
0; Mismatches 4
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                                                                                                             variants and derivs. - e in treating, preventing
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                                                                                                                                     - elicit
                                                                                                                and diagnosing
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S field.)
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The sequence was deduced from the DNA

sequence

of clone pSQ200 which

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RESULT 94
AAR10988
ID AAR1
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Best Local S
Matches 195
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Protein
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                                                                                                                                                                                                                                                                                                                                                                             25-MAR-2003
29-APR-1991
                     Claim 4; Page 45; 87pp;
                                                      New non-human primate and human CD4 or HIV or SIV and immunoglobulin and gp120
                                                                                         N-PSDB; AAQ10886.
                                                                                                    WPI; 1991-059419/09.
                                                                                                                            Seed
                                                                                                                                                                      23-AUG-1989;
                                                                                                                                                                                             18-AUG-1990;
                                                                                                                                                                                                                   27-FEB-1991.
                                                                                                                                                                                                                                          EP414178-A.
                                                                                                                                                                                                                                                                                                           Pan troglodytes
                                                                                                                                                                                                                                                                                                                                Chimpanzee; CD4;
                                                                                                                                                                                                                                                                                                                                                     Chimpanzee CD4 protein
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les 195; Conserv
  CD4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
protein
                                                                                                                                                                                                                                                                                                                                                                                                                                   standard;
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                                                                                                                         Camerini D;
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                                                                                                                                                 HOSPITAL
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(first entry)
                                                                                                                                                                      89US-00397782
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                                                                                                                                                                                                                                                                                                                                 AIDS; HIV1;
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97.5%;
HIV gp120-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                   protein;
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                      English
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Pred. No. 1.9e-61;
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                                                      gp120
fragments of
                                                      gp120 molecules - used to treat
0 binding molecules from new fus
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The sequence was deduced

from the DNA sequence of clone pSQ205 which was

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RESULT 95
AAR20150
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Best Local Sim
Matches 195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and treat HIV and SIV infection. Animals which can be treated include humans, baboons, orang-utans, chimpanzees, gorillas and thesus monkeys. The chimpanzee CD4 is 99 per cent homologous to its human counterpart, possessing 5 amino acid substitutions in the 433 residue predicted mature polypeptide. See also AAQ10885, AAQ10887-8. (Updated on 25-MAR-2003 to
                                                                                                                                                                                                                                                                        Key
Peptide
                                                                                                                                                                                                                                                                                                                              Human immunodeficiency virus; HIV; gp 120; acquired immune deficiency syndrome; AIDS: T helper lymphocytes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 458 AA;
                     Claim 15;
                                           New immuno-therapeutic human CD4 variants and derivs. production to HIV gp.120, useful in treating, prevent AIDS, ARC and HIV infections.
                                                                                                                                                                                                                                                                                                                                                                            Chimpanzee sol. CD4 sequence
                                                                                                                                                                                                                                                                                                                                                                                                 25-MAR-2003
31-MAR-1992
                                                                                        N-PSDB; AAQ20325.
                                                                                                   WPI; 1992-007200/01.
                                                                                                                        Fisher RA,
                                                                                                                                                                                            25-MAY-1990;
                                                                                                                                                                                                                                        WO9118618-A.
                                                                                                                                                                                                                                                                                                         Pan troglodytes
                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR20150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR20150 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 correct PA field.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQTK
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                     Fig
                                                                                                                        Hession
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                                                                                                                                                                                                                                                                                                                                                                                                (revised)
                    20; 179pp; English.
                                                                                                                                               INC.
                                                                                                                                                                      90US-00529186
                                                                                                                                                                                            90US-00529186
                                                                                                                                                                                                                                                                                 Location/Qualifiers
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97.5%;
                                                                                                                                                                                                                                                             signal_sequence
                                                                                                                        Burkly LC;
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Pred. No. 2.
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                                                                                                                                                                                                                                                                                                                                          ; AIDS; ARC; glycoprotein; related complex;
                                                      preventing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 458;
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                                                                  elicit AB
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                                                     diagnosing
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PF 22-JJ
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XX Infect
XX TAN
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Best Local S
Matches 194
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The fusion protein genes of the invention pref. comprises cDNA sequences which encode CD4 or a fragment which binds gp120 ligated to an expression plasmid which encodes an antibody in which the variable region of the gene gene has been deleted (see Wo87-02671). The CD4 portion of the fusion protein may comprise the complete CD4 sequence, the 370 AA extracellular region and the membrane spanning domain, or the extracellular region. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-MAR-2003
03-AUG-1992
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                                                                                                                                                                                                                                                                                                       WPI; 1989-214472/30.
N-PSDB; AAN90358.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EP325262-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-JAN-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-JAN-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-JUL-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  upstream
                                                                                                                                                                               Example;
                                                                                                                                                                                                                        Immunoglobulin-CD4 fusion proteins - used for treating infections or detecting HIV or SIV in sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                  (GEHO)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             construct which encodes CD4 linked n of the CH1 region (fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
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                                                                                                                                                                            Table 3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TWTCTVLQNQKKVEFKIDIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | IGNQGSFLTKGPSKLNDRVDSRRSLWDQGNFTLIIKNLKIEDSDTVICEVGDQKEEVQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFFLIIKNLKIEDSDTYICEVEDQKEEVQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CD4;
                                                                                                                                                                                                                                                                                                                                                                                                                                  HOSPITAL
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(first ent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89EP-00100913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunoglobulin-like molecule; HIV; SIV; therapy;
gp120; binding fragment; glycoprotein; variable
                                                                                                                                                                       Page 34-40; 68pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein;
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97.0%;
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Pred. No. 4.3e-61;
l; Mismatches 5
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RESULT 97
AAB19511
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Best Local S
Matches 194
                                                                                                                                                                                                                                                                    09-JUN-1992;
12-APR-1993;
04-FEB-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ig heavy chain is pref. from IgM, IgG1 or IgG3. The following are specifically claimed: fusion proteins planbda1, CD4Pmu, CD4Pmu (No. 67608), pCD4Plambda (No. 67609) and pCD4Elambda (No. 67610). (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                         Seed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Key
Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gp120;
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                     Example
                                                                  CD4-immunoglobulin fusion SIV.
                                                                                                                        N-PSDB;
                                                                                                                        WPI; 2000-586558/55
N-PSDB; AAA50664.
                                                                                                                                                                                                                                                                                                                                   22-JAN-1988;
23-JAN-1989;
                                                                                                                                                                                                                                                                                                                                                                                                 07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CD4; IgG1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CD4-IgG1 fusion
                                                                                                                                                                                                                             (GEHO)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         \vdash
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TWTCTVLQNQKKVEFKIDIV 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
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                                                                                                                                                                                                                             HOSPITAL
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89US-00299596.

92US-00896781.

93US-00057952.

94US-00191708.
                                                                                                                                                                                                                                                                                                                                                                                                 95US-00479353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein CH4Bgammal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CD4Bgamma1; fusion protein;
                                                                                                                                                                                                                             CORP
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97.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .616
                 39pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "IgG1 heavy
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                                                                               proteins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  616
                     English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 982; DB 1;
Pred. No. 2.9e-60;
1; Mismatches
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                                                                                   useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  region"
                                                                                 for targeting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunoglobulin; HIV; SIV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
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RESULT
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-OCT-2003
25-MAR-2003
31-MAR-1992
                                                                                                                                                                                                                                                                                                                                                   acquired
T helper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 extracellular portion of CD4, which binds to HIV gp120, linked at its C-terminus to the human IgG1 heavy chain. To obtain the fusion protein, DNA encoding CD4 was linked to IgG1 DNA at the Ban1 site downstream of the hinge region (see AAA50664). Fusion protein CD4Bgammal and a nucleic acid encoding it are claimed. Also claimed are a vector comprising the nucleic acid, and a method of producing the fusion protein in secreted form using a transformed host cell. The fusion protein may further comprise a therapeutic agent, radiolabel or NMR imaging agent. The fusion protein can be administered to an animal (including humans) for treatment of HIV or SIV infection, and can also be used in assays for HIV or SIV, imaging and tissue stains. IgG1 fusion proteins such as CD4Bgammal provide both complement-mediated and cell-mediated immunity
                                                                                                                                                                                                                                                                                                                                                                Human immunodeficiency virus; HIV; gp 120; AIDS; ARC; glycoprotein; acquired immune deficiency syndrome; AIDS related complex; monkey;
                 25-MAY-1990;
                                                25-MAY-1990;
                                                                               12-DEC-1991.
                                                                                                                                                                                               Peptide
                                                                                                                                                                                                                                Region
                                                                                                                                                                                                                                                                                    Chimeric
                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                 Macaca mulatta;
                                                                                                                                                                                                                                                                                                                                                                                                                  Sol. rhesus-human chimeric CD4 encoded by pDG100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR20154 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is that of fusion protein CD4Bgammal comprising
                                                                                                                 WO9118618-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                   helper lymphocytes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       616 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LVFCLTANSDTHLLQGQSLTLTLESPPCSSPSVQCRSPRCKNIQCCKTLSVSQLELQDSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
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(revised)
(first entry)
                 90US-00529186
                                                  90US-00529186
                                                                                                                                                                          /label=_gignal_sequence
                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                   (Rhesus)
                                                                                                                                                                                                                  /note= "rhesus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73.6%;
                                                                                                                                                "human CD4 encoded by pBG391 (US8802940)"
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                                                                                                                                                                                                               CD4 encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                  pSQ146 (AAQ20328) "
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Best Local S
Matches 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New immuno-therapeutic human CD4 variants and derivs. - elicit AB production to HIV gp.120, useful in treating, preventing and diagraphs, ARC and HIV infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1992-007200/01.
N-PSDB; AAQ20329.
                                     Domain
                                                                                                                                      Domain
                                                                                                                                                                         Key
                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                           Gelsolin; fusion protein; diagnosis; AIDS
                                                                                                                                                                                                                                                   CD4 coordinate
                                                                                                                                                                                                                                                                            25-MAR-2003
24-FEB-1992
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                                                                                                                                                                                                                                                                                                                                      AAR15149 standard;
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 Domain
                                                 Disulfide-bond
                                                                                     Domain
                                                                                                  Disulfide-bond
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                                                                                                                                                                                                                                                                                                                                                                                                                  TWTCTVLQNQKKVEFKIDIV 200
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(first entry)
                                                                                                                                                                                                                                                   system
                                         ,_aDel= second_Ig-related_domain
/note= "extracellular"
155. .184
/label= third_IG-related_domain
/note= "extracellular"
319. .395
                                    203.
                                                                                                            /label= first_Ig-related_domain
/note= "extracellular"
                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                 label= hydrophobic/secretory_signal/
                                                                                                                                                                                                                                                                                                                                      protein;
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Pred. No. 2.6e-58;
9; Mismatches 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 400;
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RESULT 100
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Best Local
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           HIV; immunotherapeutic; prophylactic; soluble T4-like polypeptide; diagnostic; p199-7 (PL mutet.rsT4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1991-353711/48.
N-PSDB; AAQ14931.
                                               Amino acid portion of
                                                                                  25-MAR-2003
01-AUG-1990
                                                                                                                                           AAP90833 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New multi-meric and hetero-multi-meric gelsolin fusion constructs - to treat and diagnose AIDS, ARC and HIV infection.
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                                                                                                                                                                                                                                                                                                                                                        1 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                  TWTCTVLQNQKKVEFKIDIV 200
                                                                                                                                                                                                                                                             LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                                                                                                                             ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RB,
                                                                                                                                                                                                                                                  LVFGLTAKCERDVVEGERVSLTLERGGGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                                                                                                                                                                                                                                                                          458 AA;
                                                                                                                                                                                                                                                                                                                                             MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                             sequence of a soluble T4-like clone p199-7 (PL mutet.rsT4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fig 3A-3D;
                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                (revised)
(first entry)
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/note="extracellular"
328. .370
396. .416
/label= hydrophobic/transmembrand
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                                                                                                                                          protein;
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                                                                                                                                                                                                                                                                                                                                                                                          Score 946; DB 2;
Pred. No. 1.1e-57;
7; Mismatches 9
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Search completed: August
Job time : 29.2483 secs
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          It is the protein sequence encoded by the rsT4 sequence. It is claimed the patent. It is useful in immunotherapeutic, prophylactic and diagnostic compans. It can be used to purify HIV from a sample. (Update on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA sequences coding for soluble T4-like immuno:therapeutic and immunosuppressive treating or detecting AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fisher RA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     tch 69.6%; So all Similarity 100.0%; lal Similarity 100.0%; lal 177; Conservative 0;
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                                                                                                                                               ESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIV
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                                                                                                                                                                                                                                                                                                                                                                            QGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSR
                                                                                                                                                                                                                               RSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTL
                                                                                                                                                                                                                                                                                                                                           QGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSR
                                                                                                               ESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIV 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Page
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ΑA;
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88US-00141649
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Pred. No. 1.1e-55;
0; Mismatches 0;
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.

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Result
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Maximum Match 100%
Listing first 125 summaries
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Perfect score:
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seq length: 2000000000
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1: /cgn2_6/ptodata/1/pubpaa/US07 PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US06 NEW PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06 NEW PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US07 NEW PUB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US07 NEW PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US08 NEW PUB.pep:*

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7: /cgn2_6/ptodata/1/pubpaa/US08 PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/US08 PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/US09 PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/US09C PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/US09C PUBCOMB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/US09C PUBCOMB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/US09C PUBCOMB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/US09C PUBCOMB.pep:*

15: /cgn2_6/ptodata/1/pubpaa/US10B PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/US10C PUBCOMB.pep:*

17: /cgn2_6/ptodata/1/pubpaa/US10C PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/US10C NEW PUB.pep:*

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18: /cgn2_6/ptodata/1/pubpaa/US09C PUBCOMB.pep:*
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US-09-939-537-29

US-10-097-044A-1

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Sequence 7, Appli
Sequence 3, Appli
Sequence 2, Appli
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Sequence 31, Appli
Sequence 29, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 5, Appli
Sequence 6, Appli
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| 131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5<br>131.5 | 1023<br>1023<br>1023<br>1023<br>1023<br>1023<br>1021<br>1021   |
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| 14 US-10-105-545-25 14 US-10-076-674-4 14 US-10-076-674-4 14 US-10-076-674-5 15 US-10-355-161A-4 15 US-10-355-161A-5 16 US-10-311-823-7 16 US-10-311-823-7 17 US-10-211-462-89 18 US-10-211-462-89 19 US-10-311-823-12 10 US-10-311-823-12 10 US-10-311-823-14 10 US-10-311-823-12 10 US-10-311-823-12 10 US-10-311-823-14 11 US-10-044-918-27 116 US-10-044-918-27 116 US-10-044-986-52 12 US-10-042-865-52 13 US-10-042-865-52 14 US-10-042-865-91 18 US-10-042-865-91 19 US-09-808-602-69 10 US-09-808-602-72 10 US-09-808-602-72 10 US-09-908-723-517  | 1 US-09-243<br>2 US-10-151<br>4 US-10-103<br>4 US-10-10-207<br>US-08-681-5<br>1 US-09-891-1<br>1 US-09-891-1<br>1 US-09-991-1<br>1 US-09-934-1<br>US-09-934-1<br>US-09-934-1<br>US-09-934-1<br>US-09-934-1<br>US-09-934-1<br>US-09-934-1<br>US-09-934-1<br>US-09-934-1<br>US-09-934-1<br>US-09-934-1<br>US-09-934-1<br>US-09-934-1<br>US-09-934-1<br>US-09-934-1<br>US-09-934-1<br>US-09-934-1<br>US-09-934-1<br>US-09-934-1<br>US-09-934-1<br>US-09-934-1 |
| sequence 25, Appli sequence 4, Appli sequence 5, Appli sequence 5, Appli sequence 5, Appli sequence 7, Appli sequence 7, Appli sequence 20, Appli sequence 21, Appli sequence 28, Appli sequence 157, App sequence 16, Appli sequence 16, Appli sequence 17, Appli sequence 17, Appli sequence 27, Appli sequence 27, Appli sequence 27, Appli sequence 27, Appli sequence 28, Appli sequence 59, Appli sequence 59, Appli sequence 58, Appli sequence 58, Appli sequence 58, Appli sequence 51, Appli sequence 51, Appli sequence 51, Appli sequence 517, Appli s  | equence 3 equence 3 equence 3 equence 1 equence 27 equence 2 equence 2 equence 3 equence 6 quence 6 quence 1 quence 1 quence 1 quence 1 equence 1 equence 3 equence 3 equence 3 equence 3 equence 3 equence 3  |

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Sequence 7, Application US/08485163
Publication No. US20020098191A1
GENERAL INFORMATION:
APPLICANT: Beaudry, Gary A.
APPLICANT: Maddon, Paul J.
TITLE OF INVENTION: CD4-GAMMA2 CD
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
CCMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: BC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/485,163
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 37690-II-1-PCT-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                        STREET: 1185 AV
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
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1185 Avenue of the Americas
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US-09-97653-517
US-09-997-658-517
US-09-997-428-517
US-09-997-428-517
US-09-990-438-517
US-09-990-711-517
US-09-990-711-517
US-09-990-437-517
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US-09-991-157-517
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US-09-990-436-517
US-09-993-687-517
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US-09-990-444-517
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; ORGANISM: homo
US-09-766-995-6
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; CELL TYPE:
US-08-485-163-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 310 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/09766995
Patent No. US2002052481A1
GENERAL INFORMATION:
APPLICANT: Graham P. Allaway et al.
APPLICANT: Graham P. Allaway et al.
TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONJ
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 2048/41215-CB/JPW/SHS
CURRENT APPLICATION NUMBER: US/09/786,995
CURRENT FILING DATE: 2001-01-22
NUMBER: PATENTION SEQ ID NOS: 9
SOFTWARE: PATENTIN Version 3.0
SEQ ID NO 6
LENGTH: 310
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Matches
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Best Local Similarity
Matches 209; Conserv
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ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                             Similarity
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                                LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                              ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                   MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
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                                                                                                                       ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
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         LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
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                                                                                                                                                                                                                                                                      78.8%;
llarity 85.7%;
Conservative
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lymphocyte
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                                                                                                                                                                                                                                                                      Score 1038; DB 9;
Pred. No. 1.3e-74;
4; Mismatches 19;
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Pred. No. 1
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                                                                                                                                                                                                                                                                                                               Length 310;
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US-08-485-163-7

ADDRESSEE:

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TWTCTVLQNQKKVEFKIDIVVLAFTVAAP-----SVFIFPPSDEQLKSGTASV

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VCLL 232

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US-08-485-163-3
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                                                                                                                                                                                                                                                                                          Query Match
Best Local &
                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/485,163
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 37690-II-1-PCT-US
TELEPHONE: (212) 278-0400
TELEPAX: (212) 391-0525
                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 432 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: |
ORIGINAL SOURCE:
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APPLICANT: Maddon, Paul J.
TITLE OF INVENTION: CD4-GAMMA2 CD4-IgG2 CHIMERAS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM:
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                                                                                                                                                                                                                                                                                            Local Similarity
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STREET: 1185 Avenue of the Americas
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TWTCTVLQNQKKVEFKIDIV----PRASALPAPPTGSALPDPQTASALPDPPPAA 230
                                                                                        LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180
                                                      LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                            ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                   MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
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                                                                                                                                                                                                                                                                                          78.4%;
88.0%;
                                                                                                                                                                                                                                                                                        Score 1032.5; DB Pred. No. 5.6e-74;
                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                           DB 8;
                                                                                                                                                                                                                                                                         10;
                                                                                                                                                                                                                                                                         Indels 17;
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Patent No. US20020052481A1

GENERAL INFORMATION:
APPLICANT: Graham P. Allaway et al.
TITLE OF INVENTION: AND USES THEREOF
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 2048/41215-CB/JPW/SHS
CURRENT APPLICATION NUMBER: US/09/766,995
CURRENT APPLICATION NUMBER: US/09/766,995
CURRENT FILING DATE: 2001-01-22
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.0
SEQ ID NO 20
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US-09-766-995-2
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Publication No. US20020098191A1
GENERAL INFORMATION:
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                  COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,163
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REGISTRATION NUMBER: 3,679-II-1
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ORGANISM: homo sapians
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MEDIUM TYPE: Floppy disk
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APPLICANT: Maddon, Paul J.
TITLE OF INVENTION: CD4-GAMMY
NUMBER OF SEQUENCES: 10
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Cooper & Dunham LLP
1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
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88.0%;
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                                                                                                                                                                                                                                     US-09-766-995-4
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                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Graham P. Allaway et al.
APPLICANT: Graham P. Allaway et al.
TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONJ
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 2048/41215-CB/JPW/SHS
CURRENT FAPLICATION NUMBER: US/09/766,995
CURRENT FILING DATE: 2001-01-22
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.0
LENGTH: 530
TYPE: PRT
ORGANISM: homo sapians
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/09766995
Patent No. US20020052481A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 207; Conserv
                                                                                                                                                                        Matches 207;
                                                                                                                                                                                                      Query Match
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 530 amino acids
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STRANDEDNESS: unknown
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121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
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                                                                                                                                                                                      Similarity
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                                                                    ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
                                                                                                                             MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
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                                               ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                            MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
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(212) 391-0525
                                                                                                                                                                        Conservative
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lymphocyte
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84.8%;
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84.8%;
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Pred. No. 1.1e
5; Mismatches
                                                                                                                                                                  Score 1030.5; DB y;
Pred. No. 1.1e-73;
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L.1e-73;
hes 21;
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TOPOLOGY: linear; MOLECULE TYPE: protein; SEQUENCE DESCRIPTION: SEQ ID NO: US-09-939-537-31
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US-09-939-537-31
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                                                                                                                                                          Matches 200;
                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 31:
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/939,537
FILING DATE: 24-Aug-2001
CLASSIFICATION: UNKnown>
                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 07/665,961
FILING DATE: 07-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Elbing, Karen L
REGISTRATION NUMBER: 35,238
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SFLL 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 203 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 14-FEB-1994
APPLICATION NUMBER: 07/847,566
FILING DATE: 06-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 08/284,391 FILING DATE: 02-AUG-1994 APPLICATION NUMBER: 08/195,395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
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OF INVENTION: TARGETED CYTOLYSIS OF HIV-INFECTED
CELLS BY CHIMERIC CD4 RECEPTOR- BE
                                                                                                                                                          Conservative
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Romeo, Charles
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100.0%; Prr
                                                                                                                                                      Score 1029; DB 10;
Pred. No. 4.1e-74;
0; Mismatches 0;
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                                                                                    ; MOLECULE TYPE: protein ; SEQUENCE DESCRIPTION: SEQ ID NO: 29: US-09-939-537-29
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                                                                                                                                                            INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 398 amino acids
TYPE: amino acid
STRANDEDNESS: single
Ouery Match 78.1%; Score 1029; DB 10; Best Local Similarity 100.0%; Pred. No. 9.7e-74; Matches 200; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/284,391
PILING DATE: 02-AUG-1994
APPLICATION NUMBER: 08/195,395
PILING DATE: 14-FEB-1994
APPLICATION NUMBER: 07/847,566
PILING DATE: 06-MAR-1992
APPLICATION NUMBER: 07/665,961
PILING DATE: 07-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: ELbing, Karen L
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00786/24
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Seed, Brian
Banapour, Babak
Romeo, Charles
Kolanus, Waldemar
TITLE OF INVENTION: TARGETED CYTOLYSIS OF HIV-INFECTED
CELLS BY CHIMERIC CD4 RECEPTOR- BEARING CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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ADDRESSEE: Clark & Elbing LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/939,537
FILING DATE: 24-Aug-2001
CLASSIFICATION: <Unknown>
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                                                                                                                                                 TOPOLOGY: linear
                                                                                                                                                                                                                                                                                              TELEFAX: 617-428-7045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Boston
                                                                                                                                                                                                                                                                                                                                                             00786/247001
                                           Length 398;
    Indels
    0
  Gaps
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; SEQUENCE DESCRIPTION: SEQ ID NO: US-10-097-044A-1
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US-10-097-044A-1
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                                                                                                     TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 07/842777
FILING DATE: 18-FEB-1992
APPLICATION NUMBER: 07/250785
FILING DATE: 28-SEP-1988
APPLICATION NUMBER: 07/104329
FILING DATE: 02-CCT-1987
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gregory, Timothy J.
TITLE OF INVENTION: Adheson Variants
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                               REGISTRATION NUMBER: 36,575
REFERENCE/DOCKET NUMBER: P0444P1C3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/10/097,044A
FILING DATE: 28-May-2002
CLASSIFICATION: <UNknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94080
COMPUTER READABLE FORM:
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FILING DATE: 1-UUN-1995
APPLICATION NUMBER: 09/236311
FILING DATE: 02-MAY-1994
APPLICATION NUMBER: 07/936190
FILING DATE: 26-AUG-1992
APPLICATION NUMBER: 07/936190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: South San Francisco
STATE: California
                                                             LENGTH: 402 amino acids
                                                                                                                                                                                             TELEPHONE: 415/225-8228
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                                                                                                                                                                                                                                                                                   NAME: Kubinec,
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Query Match Best Local Similarity

78.1%; Score 1029; DB 14; 100.0%; Pred. No. 9.8e-74;

Length 402;

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Sequence 9, Application US/09891119A
Publication No. US20040013683A1
GENERAL INFORMATION:
APPLICANT: Maddon, Paul J.
TITLE OF INVENTION: DERIVATIVES OF SOLUBLE T-4
FILLE REFERENCE: 2457-CY-B
CURRENT APPLICATION NUMBER: US/09/891,119A
CURRENT FILING DATE: 2001-06-25
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin version 3.1
SEQ ID NO 9
                                                                                                                                                                                                                                        RESULT 11
US-09-939-537-5
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US-09-891-119A-9
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                                                                                                                                                                                 Sequence 5, Application US/09939537
Publication No. US20030138410A1
GENERAL INFORMATION:
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Best Local Similarity
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TYPE: PRT
ORGANISM: human
               CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
                                                       NUMBER OF SEQUENCES: 53
                                                                                          Kolanus, TITLE OF INVENTION:
                                                                                                                                                                 APPLICANT: Seed, Brian
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                                                                                                                           Banapour, Babak
Romeo, Charles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78.1%; Score 1029; DB 11; 100.0%; Pred. No. 1.2e-73; ... Mismatches 0;
                                                                     Waldemar
TARGETED CYTOLYSIS OF HIV-INFECTED
CELLS BY CHIMERIC CD4 RECEPTOR- BEARING CELLS
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                                                                                                                                        RESULT 12
US-09-243-008-5
; Sequence 5, Application US/09243008
; Publication No. US20040005334A1
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Best Local Similarity
                                              Dilication NO. 50-1.
GENERAL INFORMATION:
APPLICANT: Seed, Brian et al.
TITLE OF INVENTION: Redirection of Cellular
Receptor Chimeras
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/284,391
FILING DATE: 02-AUG-1994
APPLICATION NUMBER: 08/195,395
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: 07/847,566
FILING DATE: 06-MAR-1992
APPLICATION NUMBER: 07/665,961
FILING DATE: 07-MAR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/939,537
FILING DATE: 24-Aug-2001
CLASSIFICATION: <Unknown>
             NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 617-428-0200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 462 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Elbing, Karen L
REGISTRATION NUMBER: 35,238
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 617-428-7045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78.1%; ilarity 100.0%; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1029; DB 10;
Pred. No. 1.2e-73;
0; Mismatches 0;
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                                                                                          Immunity
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US-09-939-537-6
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                                                                                                                                                                                                     Sequence 6, Application US/09939537
Publication No. US20030138410A1
GENERAL INFORMATION:
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Best Local Similarity
Matches 200; Conserv
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INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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FILING DATE: 02-Feb-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/394,176
FILING DATE: SEPTEMBER 11,1995
APPLICATION NUMBER: 08/203,866
FILING DATE: February 28, 1994
APPLICATION NUMBER: 07/847,566
FILING DATE: March 6, 1992
APPLICATION NUMBER: 07/665,961
FILING DATE: March 7, 1991
                                             APPLICANT: Seed, Brian
Banapour, Babak
Romeo, Charles
Kolanus, Waldemar
ITTLE OF INVENTION: TARGETED CYTOLYSIS OF HIV-INFECTED
CELLS BY CHIMERIC CD4 RECEPTOR- BEARING CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: KAPEN F. Lech, Ph.D
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00786/270001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: Wordperfect (Version 5.0)
CURRENT APPLICATION DATA:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                  181
                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180
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TYPE: amino acid
TOPOLOGY: linear
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COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78.1%; Score 1029; DB 11; llarity 100.0%; Pred. No. 1.2e-73; Conservative 0; Mismatches 0;
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US-09-243-008-6
; Sequence 6, Application US/09243008
; Publication No. US20040005334A1
; GENERAL INFORMATION:
APPLICANT: Seed, Brian et al.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 617-428-7045
TELEX: <UNKNOWN>
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: 08/284,391

FILING DATE: 02-AUG-1994

APPLICATION NUMBER: 08/195,395

FILING DATE: 14-FEB-1994

APPLICATION NUMBER: 07/847,566

FILING DATE: 06-MAR-1992

APPLICATION NUMBER: 07/665,961

FILING DATE: 07-MAR-1991

ATTORNEY/AGENT INFORMATION:

NAME: Elbing, Karen L

REGISTRATION NUMBER: 35,238

REFERENCE/DOCKET NUMBER: 00786/24

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein SEQ ID NO: 6:
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APPLICATION NUMBER: US/09/939,537
FILING DATE: 24-Aug-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 02110
COMPUTER READABLE FORM:
                     CORRESPONDENCE ADDRESS
                                          NUMBER OF SEQUENCES:
                                                                              TITLE OF INVENTION:
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
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ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 617-428-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Diskette
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                                                             Redirection of Cellular Immunity Receptor Chimeras
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ADDRESSEE: Clark & Elbing LLP

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                                                                                                                                                          Sequence 4, Application US/09939537
Publication No. US20030138410A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/243,008
FILING DATE: 02-Feb-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/394,176
FILING DATE: SEPTEMBER 11,1995
APPLICATION NUMBER: 08/203,866
FILING DATE: February 28,1994
APPLICATION NUMBER: 07/847,566
FILING DATE: March 6,1992
APPLICATION NUMBER: 07/865,961
FILING DATE: March 7,1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78.1%; Score 1029; DB 11; Local Similarity 100.0%; Pred. No. 1.4e-73; Nes 200; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: KAYEN F. LeCh, Ph.D
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00786/270001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: Wordperfect (Version 5.0)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                      Kolanus, TITLE OF INVENTION:
CORRESPONDENCE ADDRESS:
                  NUMBER OF SEQUENCES:
                                                                                                                                     APPLICANT: Seed, Brian
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COUNTRY: USA
ZIP: 02110-2804
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                                                                                                                                                                                                                                                                                                      TWTCTVLQNQKKVEFKIDIV 200
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                                                                                            Banapour, Babak
Romeo, Charles
                                   TARGETED CYTOLYSIS OF HIV-INFECTED CELLS BY CHIMERIC CD4 RECEPTOR- BEARING CELLS
                                                                             Waldemar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 532;
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TOPOLOGY: linear
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MOLECULE TYPE: protein
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SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-939-537-4
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                                                                                                                                                           US-09-243-008-4
                                                                                                                                                                              RESULT 16
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                                                 Sequence 4, Application US/09243008
Publication No. US20040005334A1
GENERAL INFORMATION:
APPLICANT: Seed, Brian et al.
TITLE OF INVENTION: Redirection of Cellular Immunity by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity Matches 200; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08/284,391
FILING DATE: 02-AUG-1994
APPLICATION NUMBER: 08/195,395
FILLING DATE: 14-FEB-1994
APPLICATION NUMBER: 07/847,566
FILING DATE: 06-MAR-1992
APPLICATION NUMBER: 07/665,961
FILING DATE: 07-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Elbing, Karen L
REGISTRATION NUMBER: 35,238
BEFERENCY/DOCUMER: 35,238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARRE: FRAETSEQ FOR WINDOWS Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/109/939,537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
CORRESPONDENCE ADDRESS:
                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                          181
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                                                                                                                                                                                                                                                                                                                       121
                                                                                                                                                                                                                                                                                                                                           121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180
                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                            61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
                                                                                                                                                                                                                                                                   TWTCTVLQNQKKVEFKIDIV 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 575 amino acids
TYPE: amino acid
STRANDEDNESS: single
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CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                   ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
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                                   Receptor Chimeras
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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RESULT 17
US-10-151-274-3
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Sequence 3, Application US/10151274
Publication No. US20030064071A1
GENERAL INFORMATION:
APPLICANT: Littman, Dan R.
APPLICANT: Kwon, Douglas S.
APPLICANT: Won, Douglas S.
APPLICANT: Geijtenbeck, Theo
TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY
TITLE OF INVENTION: CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 575 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version
SOFTWARE: Wordperfect (Version 5.0)
CURRENT APPLICATION NUMBER: US/09/243,008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEPAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 02-Feb-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/394,176
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APPLICATION NUMBER: 08/203,866
FILING DATE: February 28, 1994
APPLICATION NUMBER: 07/847,566
FILING DATE: March 6, 1992
APPLICATION NUMBER: 07/665,961
APPLICATION NUMBER: 07/665,961
FILING DATE: March 7, 1991
                                                                                                                                                                                                                                                                                                                                                                               LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
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REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00786/270001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78.1%; Score 1029; DB 11; ilarity 100.0%; Pred. No. 1.5e-73; Conservative 0; Mismatches 0;
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-103-597A-39
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US-10-103-597A-39
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TITLE OF INVENTION: Screening Methods
PILE REFERENCE: 102286.142
CURRENT APPLICATION NUMBER: US/10/103,597A
CURRENT FILING DATE: 2002-10-17
PRIOR APPLICATION NUMBER: PCT/GB00/03579
PRIOR FILING DATE: 2000-09-18
PRIOR PILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: GB 9922352.1
PRIOR PILING DATE: 1999-09-21
NUMBER OF SEQ ID NOS: 39
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SQ ID NO 3
LENGTH: 458
TYPE: PRT
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CURRENT APPLICATION NUMBER: US/10/151,274
CURRENT FILING DATE: 2002-05-20
PRIOR APPLICATION NUMBER: US/09/517,605
PRIOR FILING DATE: 2000-03-02
NUMBER OF SEQ ID NOS: 17
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Local Similarity 99.5%;
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                                   LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180
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Pred. No. 3.5e-73;
0; Mismatches 1
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Pred. No. 3.5e-73
0; Mismatches
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Sequence 39, Application US/10188444

Publication No. US20030104635A1

GENERAL INFORMATION:
APPLICANT: Jakobsen, Bent Karsten
TITLE OF INVENTION: Screening Methods
FILE REFERENCE: 102286.142 (CIP)
CURRENT APPLICATION NUMBER: US/10/188,444
CURRENT FILING DATE: 2002-07-02
PRIOR APPLICATION NUMBER: PCT/GB00/03579
PRIOR APPLICATION NUMBER: GB 992352.1
PRIOR FILING DATE: 1099-09-21
NUMBER OF SEQ ID NOS: 39
                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 20
US-10-207-655-170
US-10-207-655-170
Sequence 170, Application US/10207655
Publication No. US20030118592A1
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                                                                                                                                                  ; TYPE: PRT ; ORGANISM: Homo sapiens US-10-207-655-170
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APPLICANT: Hayden-Ledbetter, Martha S.
APPLICANT: Hayden-Ledbetter, Martha S.
TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
FILE REFERENCE: 390069.401C1
CURRENT APPLICATION NUMBER: US/10/207,655
CURRENT APPLICATION NUMBER: US/10/207,655
CURRENT FILING DATE: 2002-07-25
NUMBER OF SEQ ID NOS: 426
SOFTWARE: Patentin version 3.0
SEQ ID NO 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FASTSEQ for Windows Version 4.0 SEQ ID NO 39 LENGTH: 458
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                                                                             Matches 199;
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Best Local
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ORGANISM: Homo sapiens
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                                                                       Score 1023; DB 14;
Pred. No. 3.5e-73;
0; Mismatches 1;
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Pred. No. 3.5e-73;
0; Mismatches 1;
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                                                                                                                                                                                                                                                     Matches 198;
                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vei
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/681,219
FILING DATE: 22-JUL-1996
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
TITLE OF INVENTION:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 458 amino acids
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                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                        Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
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                                                         121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
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TWTCTVLQNQKKVEFKIDIV 200
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1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Takaaki Sato and Junn Yanagisawa
VENTION: COMPOUNDS THAT INHIBIT THE INTERACTION BETWEEN
VENTION: SIGNAL-TRANSDUCING PROTEINS AND THE GLGF
                                                                                                                                                                                                                                                     Conservative
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) 391-0525
- NO: 27:
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99.0%;
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                                                                                                                                                                                                                                                    Score 1021; DB 8;
Pred. No. 5e-73;
1; Mismatches 1;
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                                                                                                                                                                                                                                                     1;
                                                                                                                                                                                                                                                                                         Length 458;
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181

TWTCTVLQNQKKVEFKIDIV 200

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RESULT 23
US-10-092-138-25
Sequence 25, Application US/10092138
Publication No. US20030170723A1
Publication No. US20030170723A1
GENERAL INFORMATION:
APPLICANT: Sato, Taka-Aki
TITLE OF INVENTION: METHOD OF PREPARING A PROTEIN ARRAY BASED ON TITLE OF INVENTION: BIOCHEMICAL PROTEIN-PROTEIN INTERACTION
PILE REFERENCE: 65823/DPW/PT
CURRENT APPLICATION NUMBER: US/10/092,138
CURRENT FILING DATE: 2002-09-06
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 25
LENGTH: 458
TURES. DET
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Publication No. US20030203414A1

GENERAL INFORMATION: Taka-Aki
APPLICANT: Sato, Taka-Aki
APPLICANT: Yanagisawa, Junn
TITLE OF INVENTION: COMPOUNDS THAT INHIBIT INTERACTION BETWEEN
TITLE OF INVENTION: SIGNAL-TRANSDUCING PROTEINS AND THE GLGF (PDZ/DHR)
TITLE OF INVENTION: DOMAIN AND USES THEREOF
FILE REFERENCE: 48962-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/230,111C
CURRENT APPLICATION NUMBER: US/09/230,111C
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTIN NOS: 33
SOFTWARE: PATENTIN Vex. 2.1
SEQ ID NO 25
LENGTH: 458
TYPE: PRT
ORGANISM: human
US-09-230-111C-25
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                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: human
US-10-092-138-25
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US-09-230-111C-25
                                                                                  Query Match 77.5
Best Local Similarity 99.0
Matches 198; Conservative
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Best Local Similarity 99.0
Matches 198; Conservative
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                      1 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
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MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
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                                                                                                    77.5%;
99.0%;
                                                                                Score 1021; DB 14;
Pred. No. 5e-73;
1; Mismatches 1;
                                                                                                                              Length
                                                                                                                              458;
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                                                                                    Gaps
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| RESULT 25 US-10-024-329-32 ; Sequence 32, Application US/100243 ; Sequence 32, Application US/100243 ; Sequence 32, Application US/0030157063A1 ; GENERAL INFORMATION: ; APPLICANT: SANHADJI, Kamel ; APPLICANT: TOURAINE, Jean-Louis ; APPLICANT: HEROY, Pierre ; APPLICANT: MEHTALI, Majid ; TITLE OF INVENTION: Gene therapy ; FILE REFERENCE: 10993 ; CURRENT APPLICATION NUMBER: US/10 ; CURRENT APPLICATION NUMBER: US/10 ; CURRENT APPLICATION SERVINGER OF SEQ ID NOS: 33 ; SOFTWARE: PATENTION SERVINGER OF SEQ ID NOS: 33 ; SEQ ID NO 32 ; LENGTH: 448 ; ORGANISM: human SCD4 US-10-024-339-32  | Qy         1 MNRGVPF           Db         1 MNRGVPF           Db         1 ILGNQGS           Qy         61 ILGNQGS           Db         61 ILGNQGS           Qy         121 LVFGLTA           Db         121 LVFGLTA           QY         181 TWTCTVL           Db         181 TWTCTVL           Db         181 TWTCTVL | RESULT 24  US-09-891-119A-2  US-09-891-119A-2  ISEQUENCE 2, Application US/0989111  PUBLICATION NO. US20040013683A1  GENERAL INFORMATION: APPLICANT: Maddon, Paul J. APPLICANT: MINEMENCE: 24577-CY-B  CUTTLE OF INVENTION: DERIVATIVES OF FILE REPERENCE: 24577-CY-B  CURRENT FILING DATE: 2001-06-25  NUMBER OF SEQ ID NOS: 22  SOPTWARE: Patentin version 3.1  SEQ ID NO 2  LENGTH: 397  TYPE: PRT ORGANISM: Human  US-09-891-119A-2  Query Match Best Local Similarity 98.5%; Pr Matches 197; Conservative 1;  | Db 61 ILGNQGS  Qy 121 LVFGLTA  Db 131 TWTCTVL  Db 181 TWTCTVL      |
|---|---|--|--|
| 99-32 12, Application US/10024329 nn No. US20030157063A1 property of the control | MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60   | A-2 Application US/09891119A Application US/09891119A INO. US20040013683A1 ORMATION: Maddon, Paul J. Maddon, Paul J. MADDON, Paul J. MADDON, Paul J. ENCE: 24577-CY-B PELICATION NUMBER: US/09/891,119A LING DATE: 2001-06-25 SEQ ID NOS: 22 Patentin version 3.1 Pat | ILGNQGSFLTKGPSKLNDRADSRRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120  LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180 |

Gaps

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RESULT 26
US-10-097-044A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 191;
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                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                         APPLICATION NUMBER: 07/936190
PILING DATE: 26-AUG-1992
APPLICATION NUMBER: 07/842777
FILING DATE: 18-FEB-1992
APPLICATION NUMBER: 07/250785
FILING DATE: 28-SEP-1988
APPLICATION NUMBER: 07/104329
APPLICATION NUMBER: 07/104329
APPLICATION NUMBER: 02-OCT-1987
ATTORNEY/AGENT INFORMATION:
NAME: Kubinec, Jeffrey S.
REGISTRATION NUMBER: 36,575
REGISTRATION NUMBER: 36,575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 inch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gregory, Timothy J.
TITLE OF INVENTION: Adheson Variants
NUMBER OF SEQUENCES: 25
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: P0444P1C3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Capon, Daniel J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/10/097,044A FILING DATE: 28-May-2002 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 460 Point San Bruno
CITY: South San Francisco
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                   TYPE: amino acid TOPOLOGY: linear
                                                                                                                           TELEFAX: 415/952-9881
TELEX: 910/371-7168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/236311 FILING DATE: 02-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/457,918 FILING DATE: 1-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
                                                                                                                                                                    TELEPHONE: 415/225-8228
                                                           LENGTH: 434 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         360 Kb floppy disk
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US-10-073-118-26
; Sequence 26, Application US/10073118
; Publication No. US20030054554A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Ver.
SEQ ID NO 26
LENGTH: 788
                                                                                                                                                                                                                                                                                           Best Local Similarity Matches 178; Conserv
                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: BECQUART, JEROME
TITLE OF INVENTION: ALBUMIN DERIVATIVES WITH THERAPEUTIC FUNCTIONS
FILE REFERENCE: 06832.1429-03
CURRENT APPLICATION NUMBER: US/10/073,118
CURRENT FILING DATE: 2002-02-12
PRIOR APPLICATION NUMBER: 09/551,635
PRIOR APPLICATION NUMBER: 09/551,635
PRIOR FILING DATE: 2000-04-18
PRIOR APPLICATION NUMBER: 09/004,319
PRIOR APPLICATION NUMBER: 09/004,319
PRIOR APPLICATION NUMBER: 08/479,146
PRIOR FILING DATE: 1998-01-08
PRIOR PILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 08/295,078
PRIOR APPLICATION NUMBER: 08/295,078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 1989-08-03
NUMBER OF SEQ ID NOS: 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 08/121,236
PRIOR FILING DATE: 1993-09-13
PRIOR APPLICATION NUMBER: 07/955,243
PRIOR FILING DATE: 1992-10-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 788
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 1994-08-26
                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence: Protein fusion OTHER INFORMATION: prepro-HSA-V1V2
                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 07/561,879 FILING DATE: 1990-08-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FR 89 10480
                                         719
                                                                               135
                                                                                                                           659
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 144 ESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIV 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             116 RSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTL 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  177;
195
                                                                                                                                                                                                          599 LVAASQAALGLKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84 RSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTL 143
                                                                                                                                                   75 KLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKSEVQLLVFGLTANSDTHLL 134
                                                                                                                                                                                                                                  19 LPAATQG----NKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPS 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56 QGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSR 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 QGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSR
FKIDIV 200
                                                                                 QGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVE 194
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                                       QGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVE
                                                                                                                           KLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLL
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95.7%;
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Pred. No. 2.6e-63;
1; Mismatches 3;
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4.

Gaps

718

778

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APPLICANT: Devico, Anthony L.
APPLICANT: Fouts, Timothy R.
APPLICANT: Tuskan, Robert G.
APPLICANT: Tuskan, Robert G.
TITLE OF INVENTION: VIRUS COAT PROTEIN/RECEPTOR CHIMERAS AND METHODS OF USE
FILE REFERENCE: 4115-144 CIP
CURRENT APPLICATION NUMBER: US/09/934,060A
CURRENT APPLICATION NUMBER: US 09/684,026
PRIOR APPLICATION NUMBER: US 09/684,026
PRIOR APPLICATION NUMBER: US 60/158,321
PRIOR APPLICATION NUMBER: US 60/158,321
PRIOR FILING DATE: 1999-10-08
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn version 3.1
SEQ ID NO 26
LENGTH: 178
                                                                                                                                                                                                                                                            Sequence 6, Application US/09759841

Patent NO. US20010039026A1

GENERAL INFORMATION:
APPLICANT: Rickett, Graham A
APPLICANT: Perros, Manoussos
TITLE OF INVENTION: Assay Method
FILE REFERENCE: PC10348APME
CURRENT APPLICATION NUMBER: US/09/759,841
CURRENT FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: GB 0000661.9
PRIOR FILING DATE: 2000-01-12
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US-09-759-841-6
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US-09-934-060A-26
US-09-759-841-6
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                                                                                         PRIOR APPLICATION NUMBER: GB 0000663.5
PRIOR FILING DATE: 2000-01-12
PRIOR APPLICATION NUMBER: GB 0000659.3
PRIOR FILING DATE: 2000-01-12
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
            LENGTH: 370
TYPE: PRT
ORGANISM: Homo sapiens
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APPLICANT: FOULS, Timothy L.
APPLICANT: FOULS, Timothy R.
APPLICANT: Tuskan, Robert G.
APPLICANT: Tuskan, Robert G.
TITLE OF INVENTION: VIRUS COAT PROTEIN/RECEPTOR CHIMERAS AND METHODS OF U
FILE REFERENCE: 4115-144 CIP
CURRENT APPLICATION NUMBER: US/09/934,060A
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 09/684,026
PRIOR APPLICATION NUMBER: US 09/684,026
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: US 60/158,321
PRIOR FILING DATE: 2000-10-08
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin version 3.1
SEQ ID NO 13
LENGTH: 590
TYPE: PRT
ORGANIGM: Artificial Sequence
FEATURE:
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US-09-934-060A-13
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Sequence 2, Application US/09934060A
Patent No. US20020155121A1
GENERAL INFORMATION:
APPLICANT: Devico, Anthony L.
APPLICANT: Fouts, Timothy R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Synthesized construct
NAME/KEY: MISC FEATURE
LOCATION: (586)...(586)
OTHER INFORMATION: Xaa can be any amino acid
NAME/KEY: MISC FEATURE
LOCATION: (589)...(589)
OTHER INFORMATION: Xaa can be any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                              / Match 68.3%; Score 899; DB 9; 1
Local Similarity 100.0%; Pred. No. 3.7e-63;
hes 174; Conservative 0; Mismatches 0;
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RESULT 32
US-09-934-060A-4
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Best Local S
Matches 174
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PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: US 60/158,321
PRIOR FILING DATE: 1999-10-08
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/09934060A
Patent No. US20020155121A1
                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 4
LENGTH: 720
OTHER INFORMATION: Synthesized on NAME/KEY: MISC FEATURE LOCATION: (716)..(716) OTHER INFORMATION: Xaa can be an NAME/KEY: MISC FEATURE LOCATION: (719)..(719) OTHER INFORMATION: Xaa can be an OTHER 
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APPLICANT: Fouts, Timothy R.
APPLICANT: Tuskan, Robert G.
TITLE OF INVENTION: VIRUS COAT PROTEIN/RECEPTOR CHIMERAS AND METHODS OF
FILE REFERENCE: 4115-144 CIP
CURRENT APPLICATION NUMBER: US/09/934,060A
CURRENT FILING DATE: 2001-08-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 09/684,026
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: US 60/158,321
PRIOR FILING DATE: 1999-10-08
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin version 3.1
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TITLE OF INVENTION: VIRUS COAT PROTEIN/RECEPTOR CHIMERAS AND METHODS OF USE
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TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Pred. No. 4.8e-63;
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US-10-024-329-33
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US-10-024-329-33
APPLICANT: Maddon, Paul J.
TITLE OF INVENTION: DERIVATIVES OF SOLUBLE
FILE REFERENCE: 24577-CY-B
CURRENT APPLICATION NUMBER: US/09/891,119A
CURRENT FILING DATE: 2001-06-25
NUMBER OF SEQ ID NOS: 22
SOFTMARE: Patentin version 3.1
SEQ ID NO 10
                                                                                                                                            Sequence 10, Application US/09891119A Publication No. US20040013683A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 109993
CURRENT APPLICATION NUMBER: US/10/024,329
CURRENT FILING DATE: 2001-12-21
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 33
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Best Local Similarity
Matches 174; Conserv
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Best Local Similarity
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Publication No.
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APPLICANT: TOURAINE, Jean-Louis
APPLICANT: LEROY, Pierre
APPLICANT: MEHTALI, Majid
TITLE OF INVENTION: Gene therapy using anti-gp41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 881; DB 14;
Pred. No. 2.3e-62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                              7-4
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CURRENT FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: US 09/752,816
PRIOR FILLING DATE: 1996-11-21
PRIOR FILING DATE: 1996-11-21
PRIOR APPLICATION NUMBER: US 07/940,654
PRIOR FILING DATE: 1992-09-03
PRIOR FILING DATE: 1991-05-20
PRIOR APPLICATION NUMBER: US 07/326,328
PRIOR APPLICATION NUMBER: US 07/326,328
PRIOR APPLICATION NUMBER: US 07/326,328
PRIOR FILING DATE: 1989-03-21
PRIOR APPLICATION NUMBER: US 07/074,264
PRIOR APPLICATION NUMBER: US 07/074,264
PRIOR APPLICATION NUMBER: US 07/462,542
PRIOR APPLICATION NUMBER: US 07/462,542
PRIOR FILING DATE: 1980-01-09
PRIOR FILING DATE: 1990-01-09
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                                                                                                                                                                                                                               SOFTWARE: PatentIn version 3.1
SEQ ID NO 26
LENGTH: 93
TYPE: PRT
                                                                           Matches
                                                                                             Query Match
Best Local
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TITLE OF INVENTION: BIOLOGICALLY ACTIVE COMPOUNDS AND METHODS OF CONSTRUCTING
TITLE OF INVENTION: SAME
                                                                                                                                                                                                                                                                                                          Remaining Prior Application data removed - See File Wrapper or PALM NUMBER OF SEQ ID NOS: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 4040/1L492US2
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TYPE: PRT
                                                                                                                                                                      OTHER INFORMATION: synthetic peptide
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                                                                                                                                                                                                             ORGANISM: Artificial Sequence
                                                                                                                                                                                             FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                 R APPLICATION NUMBER: US 07/685,881
FILING DATE: 1991-04-15
APPLICATION NUMBER: US 07/574,391
FILING DATE: 1990-08-27
APPLICATION NUMBER: US 07/194,026
                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 1988-05-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 07/648,303 FILING DATE: 1991-01-25
                17 ALLPAATQGNKVVLGKKGDTVELTCTASQKKS1QFHWKNSNQIKILGNQGSFLTKGPSKL
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                                                                                             Similarity
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Cohen, Jeffery A.
Kieber-Emmons, Thomas
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                                                                           Conservative
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                                                                                             36.9%; Score 486; DB 14; Length 93; 100.0%; Pred. No. 3e-31;
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Pred. No. 7e-32;
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                                  NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.
SEQ ID NO 8
LENGTH: 84
TYPE: PRT
COGGANISM: Homo sapiens
FEATURE:
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US-10-125-692-10
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APPLICANT: Hayashi, Fumi
APPLICANT: Smith, Kelly
APPLICANT: Underhill, Da
APPLICANT: Ozinsky, Adri
                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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Publication No.
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                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/135,238B
CURRENT FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: 60/066,063
PRIOR FILING DATE: 1997-11-17
                                                                                                                                                                                                                                                    APPLICANT: No. US20020177565A1an, Garry P. APPLICANT: Hitoshi, Yasumichi TITLE OP INVENTION: TOSO FILE REFERENCE: A65635-1/DJB/RMS
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CURRENT FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: US 60/285,477
PRIOR FILING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 43
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TITLE OF INVENTION: TO11-Like Receptor 5 Ligands
TITLE OF INVENTION: of Use
FILE REFERENCE: P-IS 5155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 612
TYPE: PRT
ORGANISM: Homo sapiens
NAME/KEY: UNSURE
LOCATION: (11)..(14)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KILGNQG-SFLTKG--PSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKE 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MCRAISLRRLLLLLLQLSQLLAVTQGKTLVLGKEGESAELPCESSQKKITVFTWKFSDQR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NDRADSRRSLWDQGNFPLIIKNLKIEDSDTYIC
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52.8%; Pred. No. 2.5e-29;
tive 32; Mismatches 55
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US-09-997-165-2
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                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 240
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09997165 Patent No. US20020141999A1
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Best Local Similarity
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Best Local
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APPLICANT: Faislow, William C.
TITLE OF INVENTION: LIGAND FOR CD7 AND METHODS OF USE THEREOF
FILE REFERENCE: 2913-US
CURRENT APPLICATION NUMBER: US/09/997,165
CURRENT FILING DATE: 2001-11-27
PRIOR APPLICATION NUMBER: PCT/US00/14612
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                          .09-997-165-2
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OTHER INFORMATION:
NAME/KEY: UNSURE
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                                                                                                                                                                                           6 PFRHLLLVLQLAL---LPAATQGNKVVLGKK-----GDTVELTCTASQKKSIQFHWKNS
                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           D-QGNFPLIIKNLKIEDSDTYICE 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VELTCTASQK----KSIQFHWKNSNQI-KILGNQGSFLTK-GPSK---LNDRADSRRSLW
RGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVPRASALPAPPTGSALPDP
                               LKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSP 158
                                                                                              -----GLRGIYLRQLGPQPQDIIYYEDGVVPTTDRRFRGRIDFSGS---QDNLTITMHR 103
                                                                                                                            NQIKILGNQGSFLTK-GPS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VELTCTASQKXXXXKSIQFHWKNSNQIXKILGNQGSFLTKXGPSKXXXLNDRADSRRSLW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UNSURE
                                                                                                                                                           PPRLLLLPLLLALARGLPGALAAQEVQQSPHCTTVPVGASVNITCSTSG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (46) .. (48)
                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The xaa at positions 11 through 14 represents unknown amino acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The xaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              acid
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                                                                                                                                                                                                                                        25.2%; Score 332; DB 9; 36.4%; Pred. No. 1.9e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  at positions 46 through 48 amino acid.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 337; DB 9;
Pred. No. 2e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            position
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                position 41 represents an unknown amino
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                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                       Length 240;
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                                                                                                                                                                                                                         Indels 106;
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                                                                        Matches
                                                                                                            Query Match
                                                                                          Best Local
                                                                                                                                                                                                                                                                                                   TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 35:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FBSTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/99/939,537
FILING DATE: 24-Aug-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/284,391
FILING DATE: 02-AUG-1994
APPLICATION NUMBER: 08/195,395
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: 07-847,566
FILING DATE: 06-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KOlanus, Waldemar
TITLE OF INVENTION: TARGETED CYTOLYSIS OF HIV-INFECTED
CELLS BY CHIMERIC CD4 RECEPTOR- BEJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 07/665,961 FILING DATE: 07-MAR-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 617-428-0200
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                 201 PRASALPAPPTGSALPDPQTASALPDPPAASALPAALAVISFLLGLGLGVACVLARTR 258
سو
                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QTASALPDPPAASALPAALAVISFLLGLGLGVACVLARTQ 204
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                                                                                                                                                                                                                                                                                                                                                                                               NAME: Elbing, Karen L
REGISTRATION NUMBER: 35,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: MA
 PRASALPAPPTGSALPDPQTASALPDPPAASALPAALAVISFILGIGIGVACVLARTR 58
                                                                                                                                                                                                                      STRANDEDNESS: single
                                                                                                                                                                                                                                                TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 176 Federal Street
                                                                                                                                                                                                                                                                                                                                          TELEFAX: 617-428-7045
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Banapour, Babak
Romeo, Charles
                                                                                          21.9%;
                                                                        <u>.</u>
                                                                                          Score 288; DB 10;
Pred. No. 1e-15;
                                                                        Mismatches
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PRIOR APPLICATION NUMBER: US 08/752,816
PRIOR PELING DATE: 1996-11-21
PRIOR PELING DATE: 1996-11-21
PRIOR PELING DATE: 1992-09-03
PRIOR FILING DATE: 1992-09-03
PRIOR FILING DATE: 1992-09-03
PRIOR PELICATION NUMBER: US 07/702,833
PRIOR FILING DATE: 1991-05-20
PRIOR PELICATION NUMBER: US 07/326,328
PRIOR FILING DATE: 1991-03-21
PRIOR PELICATION NUMBER: US 07/326,328
PRIOR PELICATION NUMBER: US 07/42,64
PRIOR PELICATION NUMBER: US 07/462,542
PRIOR PELICATION NUMBER: US 07/462,542
PRIOR PELICATION NUMBER: US 07/648,303
PRIOR PELICATION NUMBER: US 07/655,881
PRIOR PELICATION NUMBER: US 07/574,391
PRIOR FILING DATE: 1991-04-15
PRIOR PELICATION NUMBER: US 07/574,391
PRIOR FILING DATE: 1990-08-27
                                                                                                                                                                                                                                                                                                                                                               RESULT 41
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                                                                                                                                                                                                                                                                                                                                     US-10-076-674-4
APPLICANT: Sokoll, Kenneth K.
TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
FILE REFERENCE: Immunogen Delivery System
CURRENT APPLICATION NUMBER: US/10/076,674
CURRENT FILING DATE: 2002-04-23
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 50
                                                                                                                                                                                                                                             Sequence 4, Application US/10076674
Publication No. US20030165478A1
GENERAL INFORMATION:
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Best Local Similarity
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SEQ ID NO 25
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APPLICANT: Williams,
APPLICANT: Weiner, D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Remaining Prior Application data removed NUMBER OF SEQ ID NOS: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 07/194,026 PRIOR FILING DATE: 1988-05-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: BIOLOGICALLY ACTIVE COMPOUNDS AND METHODS OF CONSTRUCTING AND US: TITLE OF INVENTION: SAME FILE REFERENCE: 4040/1L492US2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Cohen, Jeffery A. APPLICANT: Kieber-Emmons, Thom APPLICANT: Williams, Robert M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 95
                                                                                                                                                                                                                                                                                                                                                                                                                                            63 F-DRFDSKKGAWEKGSFPLIINKLKMEDSQTYIC 95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYIC 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLAVTQGKTLVLGKEGESAELPCESSQKKITVFTWKFSDQRKILGQHGKGVLIRGGSPSQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Application US/10105545
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18.1%; Score 238; DB 14; 54.3%; Pred. No. 1.8e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14;
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US-10-076-674-5
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; OTHER INFORMATION: Xaa indicates epsilon-Lys
US-10-076-674-4
                                   US-10-355-161A-4
                                                                                                                                                                                                                                                                                                                                                                                                            US-10-355-161A-4
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Publication No. US20030165478A1
GENERAL INFORMATION:
                                                                                                                                                                         SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/10355161A Publication No. US20040009897A1
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SEQ ID NO 5
LENGTH: 50
TYPE: PRT
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Best Local (
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Query Match
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                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/355,161A
CURRENT FILING DATE: 2003-01-31
PRIOR APPLICATION NUMBER: US 10/076674
PRIOR FILING DATE: 2002-02-14
NUMBER OF SEQ ID NOS: 13
                                                                                                                                                                                                                                                                                               APPLICANT: Sokoll, Kenneth K.
TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
FILE REFERENCE: Immunogen Delivery System
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Sokoll, Kenneth K.
TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
FILE REFERENCE: Immunogen Delivery System
CURRENT APPLICATION NUMBER: US/10/076,674
CURRENT FILING DATE: 2002-04-23
NUMBER OF SEQ ID NOS: 11
                                                                                                     TYPE: PRT
ORGANISM: Human
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: FEATURE:
                                              NAME/KEY: misc_feature LOCATION: (20)..(20) OTHER INFORMATION: Xaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: (20)..(20)
OTHER INFORMATION: Xaa indicates epsilon-Lys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Human FEATURE:
                                                                                                                                                          LENGTH: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 NOGSFLTKGPSKLNDRADSRRSLWDQGN 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOGSFLTKGPSKLNDRADSRRSLWDQGN 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.4%; Score 150; DB 14; llarity 100.0%; Pred. No. 8.5e-05; Conservative 0; Mismatches 0;
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                                                   Xaa indicates epsilon-Lys
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 11.48;
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,
Score 150;
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 DB 15;
Length 50;
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APPLICANT: Vinod Assundi
APPLICANT: Radoje T. Drmanac
APPLICANT: Meng-Yun Wang
APPLICANT: Meng-Yun Wang
APPLICANT: Yea-Huey Yang
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NEUROTRIMIN-LIKE
TITLE OF INVENTION: METHODS AND POLYNUCLEOTIDES
FILE REFERENCE: HYS-17CIP/US
CURRENT APPLICATION NUMBER: US/10/311,823
CURRENT FILING DATE: 2003-09-29
PRIOR APPLICATION NUMBER: OF/S22,085
PRIOR APPLICATION NUMBER: 09/532,085
PRIOR APPLICATION NUMBER: 09/532,085
PRIOR APPLICATION NUMBER: 09/560,875
PRIOR APPLICATION NUMBER: 09/560,875
PRIOR APPLICATION NUMBER: 09/560,875
PRIOR APPLICATION NUMBER: 09/560,875
PRIOR APPLICATION NUMBER: 09/496,914
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 09/496,914
PRIOR FILING DATE: 2000-02-03
NUMBER: 09/496,914
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NAME/KEY: misc feature
; LOCATION: (20)...(20)
; OTHER INFORMATION: Xaa indicates epsilon-Lys
US-10-355-161A-5
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US-10-355-161A-5
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Publication No. US20040116683A1
GENERAL INFORMATION:
APPLICANT: Bryan J. Boyle
APPLICANT: Nancy Mize
APPLICANT: Matthew Arterburn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5, Application US/10355161A
publication No. US20040009897A1
GENERAL INFORMATION:
APPLICANT: Sokoll, Kenneth K.
TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
FILE REFERENCE: Immunogen Delivery System
CURRENT APPLICATION NUMBER: US/10/355,161A
CURRENT FILING DATE: 2003-01-31
PRIOR APPLICATION NUMBER: US 10/076674
PRIOR APPLICATION NUMBER: US 10/076674
PRIOR FILING DATE: 2002-02-14
NUMBER OF SEQ ID NOS: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn version 3.1 SEQ ID NO 5
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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TYPE: PRT
ORGANISM: Human
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George Yeung
Ping Zhou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chenghua Liu
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| Qy 4 G  | Query Match<br>Best Local Si<br>Matches 56;   | RESULT 46  US-10-311-823-7  US-10-311-823-7  Sequence 7, Applicat.  Publication No. US20.  GENERAL INFORMATION:  APPLICANT: Bryan J.  APPLICANT: Mancy M.  APPLICANT: Matthew.  APPLICANT: Y. Tom.  APPLICANT: Chenghu.  APPLICANT: Chenghu.  APPLICANT: Winod A.  APPLICANT: Lichuan  APPLICANT: Lichuan  APPLICANT: Lichuan  APPLICANT: Lichuan  APPLICANT: Lichuan  APPLICANT: Meng-Yu.  APPLICANT: OF INVENTION:  FILLE REFERENCE: HYS  CURRENT APPLICATION N  PRIOR FILING DATE:  PRIOR APPLICATION N  | 65                                    | 117<br>206<br>157                             | Qy 59 I<br>Db 158 -   | Qy 4 G<br>   <br>  Db 99 G                                  | Query Match<br>Best Local Si<br>Matches 56;   | ; TYPE: PRT<br>; TYPE: PRT<br>; ORGANISM: HO<br>US-10-311-823-13 |
|---|---|--|---------------------------------------|---|---|---|---|--|
| GVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQ | h 10.6%; Score 139; DB 16; Similarity 26.3%; Pred. No. 0.015; S6; Conservative 33; Mismatches 82; | ESULT 46  S-10-311-823-7  Sequence 7, Application US/10311823  Publication No. US20040116683A1  GENERAL INFORMATION:  APPLICANT: Bryan J. Boyle APPLICANT: Watthew Arterburn APPLICANT: Watthew Arterburn APPLICANT: Y. Tom Tang APPLICANT: Y. Tom Tang APPLICANT: Vinod Asundi APPLICANT: Vinod Asundi APPLICANT: Vinod Asundi APPLICANT: Lichuan Chen APPLICANT: Lichuan Chen APPLICANT: Lichuan Chen APPLICANT: Vinod Asundi APPLICANT: Meng-Yun Wang APPLICANT: Lichuan Chen APPLICANT: Vinod Asundi APPLICANT: Vinod Marieri APPLICANTON NUMBER: US/10/311,823 CURRENT APPLICATION NUMBER: US/10/311,823 CURRENT FILING DATE: 2001-02-02 PRIOR APPLICATION NUMBER: 09/632,085 PRIOR APPLICATION NUMBER: 09/632,08 | LPLGALAQGG-TLSIPSVQARDSGYYNCTATNN 296 | EVQLLVFGLTANSDTHLLQGQSLTLTLESPFGSSPSVQCR      | IKILGNQGSFLTKGPSKLNDRADSRRSLMDQGNFPLI-IKNLKIEDSDTYICEVEDQKE-<br>          | GVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQ<br> | h 10.6%; Score 139; DB 16; Similarity 26.3%; Pred. No. 0.014; 56; Conservative 33; Mismatches 82; | 70<br>Homo sapiens<br>-13  |
| TVELTCTASQKKSIQFHWKNSNQ 58                              | Length 586; Indels 42; Gaps 9;  | TO NEUROTRIMIN-LIKE  |                                       | )CR 156<br>  <br> Сиртестрогом (150 году)<br> | KNLKIEDSDTYICEVEDQKE- 116<br>   ::  :   :  :<br>KNLRPQDYASYTCQVSVRNVC 205 | TVELTCTASQKKSIQFHWKNSNQ 58<br>                              | Length 570;<br>Indels 42; Gaps 9;   |  |

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Sequence 20, Application US/10274583
Publication No. US20030138431A1
GENERAL INFORMATION:
TITLE OF INVENTION: LRRCAPS AS MODIFIERS OF THE PILE REFERENCE: EX02-119C
CURRENT APPLICATION NUMBER: US/10/274,583
CURRENT FILING DATE: 2002-10-21
PRIOR APPLICATION NUMBER: 60/338,733
PRIOR APPLICATION NUMBER: 60/357,600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE OF INVENTION: NO. US20040005560A1el full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION UNMBER: US/10/108,260A
CURRENT FILING DATE: 2002-03-27
NUMBER OF SEO ID NOS: 5458
SOFTWARE: PatentIN Ver. 2.1
SEO ID NO 4247
LENGTH: 535
TYPE: PRT
ORGANISM: Homo sapiens
US-10-108-260A-4247
                                                                                                                                                                                                                                                       RESULT 48
US-10-274-583-20
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US-10-108-260A-4247
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Best Local Similarity
Matches 69; Conserv
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APPLICANT: HELIX RESEARCH INSTITUTE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        281 LPLGALAQGG-TLSIPSVQARDSGYYNCTATNN 312
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                                                                                                                                                                                                                                                                                                                                                       294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        108 ICEVE-----DQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRG 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     222 GIPDKAITFRLTNTTAPPALK-LSVNETLVVNPGENVTVQCLLTGGDPLPQLQWSHGPGP 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59 APGKGLEWVGLIWNDGSHKYYGDSVRGRFTISRDNSRNM-----FYLQMNSLKVEDTATY 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54 ---KNSNQIKILGNQGSFLTKGPS---KLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTY 107
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                                                                                                                                                                                                                                                                                                                                                                                             ----TWTCTV-----LQNQKKVEFKIDI------VPRASALPAPPTGSALPDPQTA 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KNIQGG-----KTLSVS-----QLELQDSG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MDTGLTWVFLVGLLRGVQSVVEIVESGGGVV--QPGTSLRLSCSASGFTFRNSAMYWVRQ 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSS
                                                                                                                                                                                                                                                                                                                                                  DTPPPCPRCPEPKSCDTPPPCPRCPA 319
                                                                                                                                                                                                                                                                                                                                                                                                                                            LGTQTYTCNVNHKPSNTKVDKRVELKTPLGDTTHTCPRCPEPKSCDTPPPCPRCPEPKSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.1%; Score 133; DB 1
21.2%; Pred. No. 0.039;
ative 49; Mismatches 1
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US-10-274-583-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 325
LENGTH: 1479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 325, Application US/10231956A Publication No. US20040053233A1 GENERAL INFORMATION:
APPLICANT: Lorens, James B.
APPLICANT: Xu, Weiduan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 2002-02-15
PRIOR APPLICATION NUMBER: 60/361,196
PRIOR FILING DATE: 2002-03-01
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn version 3.1
SEQ ID NO 20
LENGTH: 1477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Bogenberger, Jakob
APPLICANT: Holland, Sacha
APPLICANT: Rigel Pharmaceuticals, Incorporated
TITLE OF INVENTION: Modulators of Angiogenesis
FILE REFERENCE: 021044-004100US
CURRENT APPLICATION NUMBER: US/10/231,956A
CURRENT FILING DATE: 2001-08-30
NUMBER OF SEQ ID NOS: 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
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Local Similarity 26.5%;
                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
    422
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    HATAFII--VQALPQFTVTPQDRVVIEGQTVDFQCEAKGNPPPVIA 465
                                               EFKIDIVPRASALP---APPTGSALPDPQT----ASALPDPPAASA 232
                                                                                                                                     ----TLESPPGSSPSVQCRSP----RGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKV 193
                                                                                                                                                                                     LMIQNTQETDQGIYQCMAKNVAGEVKTQEVTLRYFGSPARPTFVIQPQNTEVLVGESVTL
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                                                                                            ECSATGHPPPRISWTRGDRTPLPVDPRVNITPSGGLYIQNVVQGDSGEYACSATNNIDSV
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                                                                                                                                                                                                                                                                                                                                                                   ; Score 131.5; DI
; Pred. No. 0.19;
27; Mismatches
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Sequence 125, Application US/10021660

Publication No. US20030152926A1

GENERAL INFORMATION:
APPLICANT: Murray, Richard
APPLICANT: Murray, Richard
APPLICANT: Wateon, Susan R.
APPLICANT: EOS Biotechnology, Inc.
TITLE OF INVENTION: No. US20030152926A1el Methods of Diagnosis of Angiogenesis,
TITLE OF INVENTION: Compositions and Methods of Screening for Angiogenesis
TITLE OF INVENTION: Modulators
FILE REFERENCE: 018501-000710US
CURRENT APPLICATION NUMBER: US/01/021,660
CURRENT FILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: US/09/784,356
PRIOR APPLICATION NUMBER: US/09/8637,977
PRIOR ENTING TATE: 2001-02-14
PRIOR ENTING TATE: 2001-02-14
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US-10-211-462-87
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SEQ ID NO 87
LENGTH: 1496
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Best Local Similarity
Matches 60; Conserv
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11TLE OF INVENTION: Methods of Diagnosis of Angiogenesis, Compositions and TITLE OF INVENTION: Methods of Screening for Angiogenesis Modulators FILE REFERENCE: 018501-006200US

CURRENT APPLICATION NUMBER: US/10/211,462

CURRENT FILING DATE: 2003-02-13

PRIOR APPLICATION NUMBER: US 09/784,356

PRIOR PILING DATE: 2001-02-14

PRIOR APPLICATION NUMBER: US 09/791,390

PRIOR APPLICATION NUMBER: US 09/791,390

PRIOR APPLICATION NUMBER: US 60/310,025
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PRIOR FILING DATE: 2001-11-29
NUMBER OF SEQ ID NOS: 230
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APPLICANT: Glynne, Richard
APPLICANT: Watson, Susan R.
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FILING DATE:
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FILE REFERENCE: P5014R1-PCT
CURRENT APPLICATION NUMBER: US/10/331,496A
CURRENT FILING DATE: 2002-12-30
PRIOR APPLICATION NUMBER: US 60/345,444
PRIOR FILING DATE: 2002-01-02
PRIOR PPLICATION NUMBER: US 60/351,885
PRIOR FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: US 60/360,066
PRIOR APPLICATION NUMBER: US 60/362,004
PRIOR PILING DATE: 2002-03-05
PRIOR PILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/366,869
PRIOR APPLICATION NUMBER: US 60/366,869
PRIOR APPLICATION NUMBER: US 60/366,869
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SEQ ID NO 125
LENGTH: 1496
TYPE: PRT
ORGANISM: Homo sapiens
                        SEQ ID NO 28
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Best Local
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                                                                                                                         PRIOR FILING DATE: 2002-03-20
PRIOR APPLICATION NUMBER: US 60/366,284
PRIOR FILING DATE: 2002-03-21
PRIOR APPLICATION NUMBER: US 60/368,679
PRIOR APPLICATION NUMBER: US 60/404,809
PRIOR FILING DATE: 2002-08-19
PRIOR FILING DATE: 2002-08-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: FRANTZ, GRETCHEN
APPLICANT: HILLAN, KENNETH
APPLICANT: PHILLIPS, HEIDI
APPLICANT: POLAKIS, PAUL
APPLICANT: SMITH, VICTORIA
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                                                 NUMBER OF SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND TITLE OF INVENTION: TREATMENT OF TUMOR
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                                                                        PRIOR FILING DATE:
                                                                                                   PRIOR APPLICATION NUMBER: US
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LENGTH:
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                                                                             2002-08-21
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DB 15;

Length 1496,

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RESULT 54
US-10-243-552-899
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US-10-276-774-1957
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Sequence 899, Application US/10243552
Publication No. US20030224379A1
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Zhiwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 09/496,914
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 2700
SOFTWARE: CUSCOM
SEQ ID NO 1957
LENGTH: 1498
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Publication No. US20040053245A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
APPLICANT: Tang, Y, Tom et al
TITLE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-030
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Best Local S
Matches 60
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Best Local :
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CURRENT FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: 09/560,875
PRIOR FILING DATE: 2000-04-27
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26.5%; Pred. No. 0.19;
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Pred. No. 0.19;
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:

Y. Tom Tang George Yeung Ping Zhou Chenghua Liu

Matthew Arterburn

APPLICANT: APPLICANT:

APPLICANT:

Vinod Asundi Radoje T. Drmanac Meng-Yun Wang Lichuan Chen

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RESULT 55
US-10-311-823-16
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APPLICANT: Ma, Yunqing
ITITLE OF INVENTION: Novel Nucleic Acids and
ITITLE OF INVENTION: Polypeptides
FILE REFERENCE: 807A
CURRENT APPLICATION NUMBER: US/10/243,552
CURRENT FILING DATE: 2002-09-12
PRIOR APPLICATION NUMBER: US 60/322,511
PRIOR APPLICATION NUMBER: US 60/322,511
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: PCT/US01/03600
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: PCT/US01/03600
PRIOR FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: US 09/496,914
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: PCT/US01/04927
PRIOR APPLICATION NUMBER: PCT/US01/04927
PRIOR APPLICATION NUMBER: PCT/US01/04927
PRIOR FILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: PCT/US01/04927
PRIOR FILING DATE: 2001-02-26
PRIOR FILING DATE: 2001-02-26
PRIOR FILING DATE: 2001-04-27
PRIOR FILING DATE: 2001-02-26
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Sequence 16, Application US/103
Publication No. US20040116683A1
GENERAL INFORMATION:
APPLICANT: Bryan J. Boyle
APPLICANT: Nancy Mize
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SOFTWARE: pt_FL_genes Version 5.0
SEQ ID NO 899
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Local Similarity 26.5%; Pred. No. 0.19;
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                                                                                                            Application US/10311823
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                                                                                        PRIOR APPLICATION NUMBER: PCT/US01/03651
PRIOR FILING DATE: 2001-02-02
PRIOR PPLICATION NUMBER: 09/632,085
PRIOR FILING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: 09/560,875
PRIOR APPLICATION NUMBER: 09/496,914
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 09/496,914
PRIOR FILING DATE: 2000-02-03
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PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 09/632,085
PRIOR FILING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: 09/560,875
PRIOR APPLICATION NUMBER: 09/496,914
PRIOR APPLICATION NUMBER: 09/496,914
PRIOR FILING DATE: 2000-02-03
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 16
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SOFTWARE: PatentIn Ver.
SEQ ID NO 12
LENGTH: 442
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Best Local Similarity
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APPLICANT:
APPLICANT:
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CURRENT FILING DATE: 2003-09-29
                                                                       PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 16
                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/311,823
CURRENT FILING DATE: 2003-09-29
                                                                                                                                                                                                                                                                                                                                     APPLICANT: Yea-Huey Yang
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NEUROTRIMIN-LIKE
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
FILE REFERENCE: HYS-17CIP/US
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Radoje T. Drmanac
Meng-Yun Wang
Lichuan Chen
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Chenghua Liu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         George Yeung
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Y. Tom Tang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Boyle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9.9%; Score 131; DB 16; Length 374;
27.3%; Pred. No. 0.036;
ative 25; Mismatches 67; Indels 3
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                                                                                                                                                                                                                                                                                                                                                ; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-311-823-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: HYS-17CIP/US
CURRENT APPLICATION NUMBER: US/10/311,823
CURRENT FILING DATE: 2003-09-29
PRIOR APPLICATION NUMBER: PCT/US01/03651
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 09/632,085
PRIOR FILING DATE: 2000-08-02
PRIOR FILING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: 09/560,875
PRIOR APPLICATION NUMBER: 09/496,914
PRIOR APPLICATION NUMBER: 09/496,914
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 16
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APPLICANT: Mancy Mize
APPLICANT: Matthew Arterbu
APPLICANT: Y. Tom Tang
APPLICANT: George Yeung
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                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/10311823 Publication No. US20040116683A1
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                        152 SVQC--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184 KLKNIRPODYASYTCOVSVRNVCGIPDKAITFRITNTTAPPAIK-ISVNETIVVNPGENV
                                                                     200 KLKNIRPQDYASYTCQVSVRNVCGIPDKAITFRITNTTAPPALK-LSVNETLVVNPGENV
                                                                                                                                                              152 TVFLRCTVNSNPPARFIWKRGSD------TLSHSQDNG-VDIYEPLYTQGETKVL 199
                                                                                                                 96 -IKNIKIEDSDTYICEVEDQKE---EVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSP 151
                                                                                                                                                                                                       36 TVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLI 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96 - IKNIKIEDSDTYICEVEDQKE---EVQLIVFGLTANSDTHLLQGQSLTLTLESPPGSSP 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36 TVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLI 95
                                                                                                                                                                                                                                                          48;
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Chenghua Liu
Vinod Asundi
Radoje T. Drmanac
Meng-Yun Wang
Lichuan Chen
Yea-Huey Yang
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                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                  9.9%; Score 131; DB 16; 27.3%; Pred. No. 0.046; ative 25; Mismatches 67;
----RSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQN 189
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                                                                                                                                                                                                                                                                                                  Length 458;
                                                                                                                                                                                                                                                       Indels 36;
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259

TVQCLLTGGDPLPQLQWSHGPGPLPLGALAQGG-TLSIPSVQARDSGYYNCTATNN 313

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RESULT 59
US-10-650-509-27
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; OTHER INFORMATION: the sixth Ig-like domain of the cell adhesion molecule US-10-024-918-27
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TITLE OF INVENTION: ENZYME-MEDIATED MODIFICATION OF FIBRIN FOR TISSUE ENGINEERING
FILE REFERENCE: CIT 2606 CIP
CURRENT APPLICATION NUMBER: US/10/024,918
CURRENT FILING DATE: 2001-12-18
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin version 3.1
SEQ ID NO 27
LENGTH: 1260
           APPLICATI: Hall, Heike
APPLICATI: Hall, Heike
TITLE OF INVENTION: ENZYME-MEDIATED MODIFICATION OF FIBRIN FOR TISSUE ENGINEERING
FILE REFERENCE: CIT 2606 CIP CON
CURRENT APPLICATION NUMBER: US/10/650,509
CURRENT FILING DATE: 2003-08-27
PRIOR APPLICATION NUMBER: 10/024,918
PRIOR FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: 09/057,052
PRIOR PRIOR APPLICATION NUMBER: PCT/US98/06617
PRIOR APPLICATION NUMBER: PCT/US98/06617
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/042,143
PRIOR FILING DATE: 1999-04-03
PRIOR FILING DATE: 1997-04-03
PRIOR FILING DATE: 1997-04-03
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Publication No. US20020168718A1
GENERAL INFORMATION:
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Publication No. US20040082513A1
GENERAL INFORMATION:
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Best Local
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FEATURE:
NAME/KEY: MISC FEATURE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            170 SVSQLELQDSGTWTCTVLQNQKKVE--FKIDIVPRASALPAPPTGSALPDPQTA 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124 GLTAN-----SDTHLLQGQSLTLTLESPPGSSPSVQCRSP------RGKNIQGGKTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          558 -----DLQERGDSDKYFIEDGK--LVIQSLDYSDQGNYSCVASTELDEVESRAQLLVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            507 ILANLQVKEATQITQGPRSAIEKKGARVTFTCQASFDPSLQASITWRGDGR------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 LLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQ--FHWKNSNQIKILGNQGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68 FLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYIC----EVEDQKEEVQLLVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 23.9
56; Conservative
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Zisch, Andreas
Hall, Heike
PatentIn version 3.1
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Til, Heike
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Pred. No. 0.17;
33; Mismatches
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US-10-650-509-27
US-10-094-886-52
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NAME/KEY: MISC FEATURE
LOCATION: (516)..(604)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Mus Musculus
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                                                                                                           SVSQLELQDSGTWTCTVLQNQKKVE--FKIDIVPRASALPAPPTGSALPDPQTA 221
                                                                        SLGKV----PGNQTSTTLKLSPYVHYTFRVTAINKYGPGEPSPVSESVVTPEAA 712
                                                                                                                                                   GSPGPVPHLELSDRHLLKQSQVHLSW-----SPAEDHNSPIEKYDIEFEDKEMAPEKWF
                                                                                                                                                                                   GLTAN-----SDTHLLQGQSLTLTLESPPGSSPSVQCRSP-----RGKNIQGGKTL 169
                                                                                                                                                                                                                          ----DLQERGDSDKYFIEDGK--LVIQSLDYSDQGNYSCVASTELDEVESRAQLLVV 608
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Pred. No. (
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APPLICANT:
APPLICANT:
APPLICANT:
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                           APPLICANT: Zhong, Mei
TITLE OF INVENTION: THERAPEUTIC POLYPEPTII
FILE REFERENCE: 21402-290 B
CURRENT APPLICATION NUMBER: US/10/094,886
CURRENT FILING DATE: 2002-03-07
PRIOR APPLICATION NUMBER: 60/274,322
PRIOR FILING DATE: 2001-03-08
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APPLICATION NUMBER: 60/313,182 FILING DATE: 2001-08-17
                                                                                                                                           Rastelli, Luca
Spaderna, Steven
LaRochelle, William
                                                                                                                                                                                              Fernandes, Blma
Shimkets, Richard
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                                                                                                                                                                                                                                                                Smithson, Glennda
Zerhusen, Bryan
                                                                                                                                                                                                                                                                                                                   Gangolli, Esha
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Taupier, Raymond J.,
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Burgess, Catherine
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                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 38, Appropriate Publication No.
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                               APPLICANT
                                                                                                        APPLICANT
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TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/296,693
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APPLICATION NUMBER: 60/313,626
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                                                                                                                                                                                                                                                                                                                                                                                                         Application US/10094886
Fernandes, Elma
Shimkets, Richard
                           Gerlach, Valeri
Pochart, Pascal
                                         Smithson, Glennda
Zerhusen, Bryan
Gerlach, Valerie
                                                                                     Gangolli, Esha
Gusev, Vladimir
                                                                                                                                                                                                                                                                                                                                 Spytek, Kimberly A.
                                                                                                                                                Miller,
                                                                                                                                                                              Padigaru,
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Malyankar, Uriel M.
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                                                                                                                                                                                                                                                                                      Corine A.
                                                                                                                                  Stacie
                                                                                                                                                  Charles
                                                                                                                                                                Raymond J.,
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US-09-808-602-69
, Sequence 69, Application User Patent No. US20020155115A1
, GENERAL INFORMATION:
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US-10-094-886-38
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LENGTH: 1386
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Best Local (
              CURRENT APPLICATION NUMBER: US/09/808,602
CURRENT FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 09/800,198
                                                                                    APPLICANT: Fernandes, Elma
APPLICANT: Shimkets, Richard A
APPLICANT: Herrman, John L
APPLICANT: Majunder, Kumud
APPLICANT: Majunder, Kumud
APPLICANT: Mezes, Peter S
APPLICANT: Mezes, Peter S
APPLICANT: MacDougall, John
TITLE OF INVENTION: No. US20020155115A1el Proteins
FILE REFERENCE: 15966-697 CIP
                                                                                                                                                                                                                        APPLICANT: Vernet, Corine A
APPLICANT: Fernandes, Elma
APPLICANT: Shimkets, Richai
APPLICANT: Herrman, John L
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PRIOR FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: 60/288,052
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/318,510
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PRIOR FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 60/296,693
PRIOR FILING DATE: 2001-06-07
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CURRENT FILING DATE: 2002-03-07
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TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC
PRIOR FILING DATE:
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Spaderna, Steven
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larity 27.3%; Pred. No. 0.19;
Conservative 25; Mismatches
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PRIOR APPLICATION NUMBER: 2001-03-05
PRIOR APPLICATION NUMBER: 60/186,596
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 98
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 58
LENGTH: 338
TYPE: PRT
GRGANISM: Homo Bapiens
US-09-800-198-58
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US-09-808-602-69
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US-09-800-198-58
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Matches 57
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Best Local :
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APPLICANT:
APPLICANT:
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APPLICANT: Mezes, Peter S
APPLICANT: Rastelli, Luca
TITLE OF INVENTION: MOVEL PROTEINS AND NUCLEIC
FILE REPERENCE: 15966-697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Vernet,
APPLICANT: Fernanc
APPLICANT: Shimket
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CURRENT FILING DATE: 2001-03-05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14 LVLLRLLCLLPTGLPVRSVDFNRGTDNITVRQGDTAILRCVLEDKNS-KVAWLNRSGIIF 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 LLLVLQLALLPAA-----TQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKI
                                   62 LGNQGSFLTKGPSKLNDRA--DSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKE--- 116
                                                                            14 LVLLRLLCLLPTGLPVRSVDFNRGTDNITVRQGDTAILRCVLEDKNS-KVAWLNRSGIIF
                                                                                                                 10 LLLVLQLALLPAA-----TQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKI 61
                                                                                                                                                          57;
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                                                                                                                                                    h 9.8%; Score 129; DB 10; Length 338; Similarity 23.2%; Pred. No. 0.045; 57; Conservative 40; Mismatches 91; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fernandes, Elma
Shimkets, Richard A
Herrmann, John L
Majumder, Kumud
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AGHD-----KWSLDPRVELEKRHSL----EYSLRIQKVDVYDEGSYTCSVQTQHEPKT 121
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23.2%; Pred. No. 0.045;
ative 40; Mismatches
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                                                                                                                                                          Indels 58;
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RESULT 64
US-10-042-865-92
; Sequence 92, Application US/10042865
; Publication No. US20040029216A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Li, Li
; APPLICANT: Li, Li
                                                                                                   TITLE OF INVENTION: Using the Same
FITTLE REFERENCE: 21402-537
CURRENT APPLICATION NUMBER: U$/10/042,865
CURRENT FILING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: 60/260,417
PRIOR FILING DATE: 2001-01-09
PRIOR FILING DATE: 2001-01-09
PRIOR FILING DATE: 2001-01-10
PRIOR PILING DATE: 2001-01-03
PRIOR PILING DATE: 2001-02-28
PRIOR FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 60/274,876
PRIOR APPLICATION NUMBER: 60/284,704
PRIOR FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 60/284,704
PRIOR FILING DATE: 2001-04-18
NUMBER OF SEQ ID NOS: 264
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; ORGANISM: Homo sapiens
US-10-042-865-92
                                                SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 92
LENGTH: 338
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APPLICANT:
APPLICANT:
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                                    TYPE: PRT
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Peyman, John
Smithson, Glennda
Gunther, Erik
Stone, David
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Gerlach, Valerie L
Edinger, Shlomit R
Rochenberg, Mark B
Ellerman, Karen
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Malyankar, Uriel M
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Gangolli, Esha A
Burgess, Catherine
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Shenoy, Suresh G
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Grosse, William
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Miller, Charles E
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Taylor, Sarah
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Zerhusen, Bryan D
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William M
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Query Match Best Local Similarity

9.8%; 23.2%;

Score 129; DB 12; Pred. No. 0.045;

Length 338;

Matches

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; TYPE: PRT ; ORGANISM: Homo sapiens US-10-161-572-58
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US-10-161-572-58
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Publication No. US20030087266A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 58
                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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TITLE OF INVENTION: IGS AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE FILE REFERENCE: EX02-097C-PC
CURRENT APPLICATION NUMBER: US/10/161,572
CURRENT FILING DATE: 2002-06-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 63
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/296,076
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/328,605
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FILING DATE: 2002-02-15
APPLICATION NUMBER: US 60/357,600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                      204
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                                                                                                                                                                        117 -EVQLLVFG----LTANSDTHLLQGQSLTLTLESPPGSSPSVQCR--SPRGKNIQGGKT- 168
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                                                                                                                                                                                                            73 AGHD------KWSLDPRVELEKRHSL----EYSLRIQKVDVYDEGSYTCSVQTQHEPKT 121
                                                                                                                                                                                                                                                    62 LGNQGSFLTKGPSKLNDRA--DSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKE---
                                                                                                                                                                                                                                                                                          14 LVLLRLLCLLPTGLPVRSVDFNRGTDNITVRQGDTAILRCVLEDKNS-KVAWLNRSGIIF
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SALPAP 209
                                                          LEILGITREQSGKYECKAANEVSSADVKQVKVTVNYPPTITESKSNEATTGRQASLKCEA
                                                                                            LSVSQLELQDSGTWTCTVLQ-----NQKKVEFKIDIVP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SAVPAP 247
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23.2%; Pred. No. 0.045;
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US-10-038-854-158
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Ş
                                                                                                                ; TYPE: PRT ; ORGANISM: Homo sapiens US-10-038-854-158
                                                                                                                                                                    SOFTWARE: Pater
SOFTWARE: Pater
; SEQ ID NO 158
***FINGTH: 338
                                                        Query Match
Best Local (
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                                      Matches
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PRIOR FILING DATE: 2000-12-29
PRIOR APPLICATION NUMBER: 60/259,415
PRIOR FILING DATE: 2001-01-02
PRIOR APPLICATION NUMBER: 60/259,785
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CURRENT FILING DATE: 2003-01-22
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TITLE OF INVENTION: Proteins and Nucleic Acids Encoding
FILE REFERENCE: 21402-230
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PRIOR FILING DATE: 2001-03-29
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                                    l Similarity
57; Conserv
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Etsen, Andrew J
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Gusev, Vladimir Y
Gangolli, Esha A
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Gunther, Erik
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Edinger, Shlomit R
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Rastelli, Luca
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Shimkets, Richard A
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Millet, Isabelle
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Boldog, Ferenc
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                                      Conservative
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23.2%;
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US-09-808-602-72
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Best Local S
Matches 56
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SEQ ID NO 72
LENGTH: 338
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Rattus norvegicus -09-808-602-72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: MacDougall, John
TITLE OF INVENTION: No. US20020155115A1el Proteins and Nuclec Acids Encoding
FILE REFERENCE: 15966-697 CIP
CURRENT APPLICATION NUMBER: US/09/808,602
CURRENT FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 09/800,198
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/186,596
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 114
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             242
                                          204 SALPAP 209
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                                                                                                                                122 SQVYLIVQVPPKISNISSDVTVNEGSNVTLVCMANGRPEPVITWRHLTPLGREFEGEEEY 181
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                                                                                                                                                                                                                   62 LGNQGSFLTKGPSKLNDRA--DSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKE---
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                                                                                                                                                                                                                                                                             10 LLLVLQLALLPAA-----TQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKI
                                                                                                                                                                                                                                                                                                           Similarity 22.6
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Majumder, Kumud
Mishra, Vishnu
Mezes, Peter S
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                                                                      LEILGITREQSGKYECKAANEVSSADVKQVKVTVNYPPTITESKSNEATTGRQASLKCEA 241
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Shimkets, Richard A
             247
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22.6%; Pred. No. 0.079;
7ative 41; Mismatches
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US-10-042-865-91
Sequence 91, Application US/10042865
Publication No. US20040029216A1
GENERAL INFORMATION:
APPLICANT: Padigaru, Muralidhara
APPLICANT: Li, Li
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US-09-800-198-61
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SEQ ID NO 61
LENGTH: 338
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Best Local Similarity
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APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT: Fernanda
APPLICANT: Shimker
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                             APPLICANT
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                                                                              Spytek, Kimberly
Zhong, Mei
Gangolli, Esha A
Burgess, Catherine E
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Majumder, Kumud
Mishra, Vishna
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Shimkets, Richard
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No. US20030087816A1
       Tchernev, Veliza
Miller, Charles
                                                                                                                                           Casman, Stacie J
Shenoy, Suresh G
                                         Vernet, Coring
Taylor, Sarah
                                                                      Patturajan, Meera
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Xiaojia
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                           Velizar
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CURRENT APPLICATION NUMBER: US/09/800,198
CURRENT FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: 60/186,596
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 98
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APPLICANT: Mezes, Peter S
APPLICANT: Restelli, Luca
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 15966-697
                                                                                                                                                                                        117 -EVQLLVFG----LTANSDTHLLQGQSLTLTLESPPGSSPSVQCR--SPRGKNIQGGKT- 168
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                                                                                                                         SQVYLIVQVPPKISNISSDVTVNEGSNVTLVCMANGRPEPVITWRHLTPLGREFEGEEEY
LEILGITREQSGKYECKAANEVSSADVKQVKVTVNYPPTITESKSNEATTGRQASLKCEA
                                                           LSVSQLELQDSGTWTCTVLQ-----NOKKVEFKIDIVP-----
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Pred. No. 0.079;
1; Mismatches 91;
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Sequence 14, App...

Sequence 14, App...

Publication No. US2004uv...

GENERAL INFORMATION:

APPLICANT: Padigaru, Muralidhara
APPLICANT: Li, Li

APPLICANT: Zerhusen, Bryan D

APPLICANT: Casman, Stacie J

APPLICANT: Shenoy, Suresh G

TTANT: Spytek, Kimberly
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US-10-042-865-14
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PRIOR FILING DATE: 2001-01-09
PRIOR APPLICATION NUMBER: 60/260,831
PRIOR FILING DATE: 2001-01-10
PRIOR APPLICATION NUMBER: 60/272,338
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: 60/274,876
PRIOR APPLICATION NUMBER: 60/274,876
PRIOR PILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 60/284,704
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Best Local :
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APPLICANT: Gunther, Erik
APPLICANT: Stone, David
TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods
TITLE OF INVENTION: Using the Same
FILE REFERENCE: 21402-537
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CURRENT FILING DATE: 2002-05-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14 LVLLRLLCLLPTGLPVRSVDFNRGTDNITVRQGDTAILRCVVEDKNS-KVAWLNRSGIIF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                     SALPAP 209
                                                                                                                                                                                                                                                                                                                                                       LEILGITREQSGKYECKAANEVSSADVKQVKVTVNYPPTITESKSNEATTGRQASLKCEA
                                                                                                                                                                                                                                                                                                                                                                                          LSVSQLELQDSGTWTCTVLQ-----NQKKVEFKIDIVP------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              -EVQLLVFG----LTANSDTHLLQGQSLTLTLESPPGSSPSVQCR--SPRGKNIQGGKT- 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGHD-----KWSLDPRVELEKRHAL----EYSLRIQKVDVYDEGSYTCSVQTQHEPKT
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Edinger, Shlomit R
Rothenberg, Mark E
Ellerman, Karen
                                                                                                                                                                     Application US/10042865
No. US20040029216A1
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Grosse, William M
Alsobrook II, John
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Peyman, John
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Malyankar, Uriel M
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Pred. No. 0.079;
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CURRENT FILING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: 60/260,417
PRIOR FILING DATE: 2001-01-09
PRIOR APPLICATION NUMBER: 60/260,831
PRIOR FILING DATE: 2001-01-10
PRIOR PELICATION NUMBER: 60/272,338
PRIOR APPLICATION NUMBER: 60/274,876
PRIOR APPLICATION NUMBER: 60/274,876
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LENGTH: 354
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TITLE OF INVENTION: Proteins, Polynucleotides
TITLE OF INVENTION: Using the Same
FILE REFERENCE: 21402-537
FILE REFERENCE: 21402-537
                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 35
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Local Similarity 23.0%;
les 53; Conservative 3
                                185 TV----- LQNQKKVEFKIDIVPRASALPAPPT-------GSALPDP 218
                                                                     144 ISNDMTVNEGTNVTLTCLATGKPEPSISWRHISPSAKPFENGQYLDIYGITRDQAGEYEC
                                                                                                  128 -NSDTHLLQGQSLTLTLESPPGSSPSVQCR--SPRGKNIQGGKTLSVSQLELQDSGTWTC 184
204 SAENDVSFPDVRKVKVVVNFAPTIQEIKSGTVTPGRSGLIRCEGAGVPPP 253
                                                                                                                                         96 LNKR------DYSLQIQNVDVTDDGPYTCSVQTQHTPRTMQVH-LTVQVPPKIYD 143
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                                                                                                                                                                    LNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTA----- 127
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Gerlach, Valerie L
Edinger, Shlomit R
Rothenberg, Mark E
Ellerman, Karen
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Gunther, Erik
Stone, David
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Malyankar, Uriel
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Grosse, William
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Gangolli, Esha A
Burgess, Catherine
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Taylor, Sarah
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harles E
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Pred. No. 0.083;
37; Mismatches
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US-09-989-722-517
Sequence 517, Application US/09989722
Patent No. US20020072067A1
GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J

60/088738

60/088217

60/088202

60/088212

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PRIOR
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C63
CURRENT APPLICATION NUMBER: US/09/989,722
CURRENT FILING DATE: 2001-11-19
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OR FILING DATE: 1998-05-28
OR APPLICATION NUMBER: 60/087607
OR APPLICATION NUMBER: 60/087609
OR APPLICATION NUMBER: 60/087609
OR FILING DATE: 1998-06-02
OR APPLICATION NUMBER: 60/087759
OR APPLICATION NUMBER: 60/087827
OR APPLICATION NUMBER: 60/087827
OR APPLICATION NUMBER: 60/087827
OR APPLICATION NUMBER: 60/088021
OR APPLICATION NUMBER: 60/088021
OR APPLICATION NUMBER: 60/088025
OR APPLICATION NUMBER: 60/088025
OR APPLICATION NUMBER: 60/088025
OR FILING DATE: 1998-06-04
OR APPLICATION NUMBER: 60/088026
OR FILING DATE: 1998-06-04
OR APPLICATION NUMBER: 60/088026
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OR APPLICATION NUMBER: 60/088026
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FILING DATE: 1997-06-16
DR APPLICATION NUMBER: 60/062250
DR FILING DATE: 1997-10-17
DR APPLICATION NUMBER: 60/065186
DR FILING DATE: 1997-11-12
DR APPLICATION NUMBER: 60/065311
    OR FILING DATE: 1998-06-04

R APPLICATION NUMBER: 60/088029

R FILING DATE: 1998-06-04

OR APPLICATION NUMBER: 60/088030

R FILING DATE: 1998-06-04

R APPLICATION NUMBER: 60/088033

OR FILING DATE: 1998-06-04

OR APPLICATION NUMBER: 60/088326

OR APPLICATION NUMBER: 60/088167
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REFILING DATE: 1998-03-20
DR APPLICATION NUMBER: 60/083322
REFILING DATE: 1998-04-28
DR APPLICATION NUMBER: 60/084600
DR APPLICATION NUMBER: 60/084600
DR FILING DATE: 1998-05-07
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APPLICATION NUMBER: 60/075945
PTITING DATE: 1998-02-25
CO/078910
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APPLICATION NUMBER: 60/066770
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Gerber, Hanspeter
Gerritsen, Mary E.
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Botetein, David
Desnoyers, Luc
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Williams,
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art, Timothy A.
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P. Mickey
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FILING DATE: 1998-07-02
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                                         AQQTQPPGLTSPGLYPAATTAKQGKTGAEAPPLPGTSQYGHERTSQYTGTSPHPATSPPA
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PRIOR FILING DATE: 1997-06-16
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and
TITLE OF INVENTION: Acide Encoding the Same
FILE REFERENCE: P2730P1C62
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APPLICATION NUMBER: 60/065186
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APPLICATION NUMBER: 60/065311
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FILING DATE: 1998-06-02
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FILING DATE: 1998-02-25
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Stewart, Timothy A.
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Botstein, David
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OR APPLICATION NUMBER: 60/090429
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OR APPLICATION NUMBER: 60/090431
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60/089512 60/089440 NUMBER: 60/089105

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| APPLICANT: Gurmay, Austin L. APPLICANT: Rajacr, Mary A. APPLICANT: Rajacr, Mary A. APPLICANT: Rajacr, Mary A. APPLICANT: Pani, Micholas F. APPLICANT: Stewart, Tinchty A. APPLICANT: Stewart, Tinchty A. APPLICANT: Stewart, Tinchty A. APPLICANT: Stewart, Tinchty A. APPLICANT: Malanabe, Colin K. APPLICANT: Williams, P. Mickey APPLICANT: Williams, P. Williams, P. Williams, P. Micke | 0 U S   |
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| PRIOR FILING DATE: 1998-06-10 PRIOR REPLICATION NUMBER: 60/088738 PRIOR FILING DATE: 1998-06-10 PRIOR APPLICATION NUMBER: 60/088742 PRIOR FILING DATE: 1998-06-10 PRIOR APPLICATION NUMBER: 60/088810 PRIOR APPLICATION NUMBER: 60/088824 PRIOR FILING DATE: 1998-06-10 PRIOR APPLICATION NUMBER: 60/088826 PRIOR FILING DATE: 1998-06-11 PRIOR APPLICATION NUMBER: 60/088861 PRIOR FILING DATE: 1998-06-11 PRIOR PRILING DATE: 1998-06-11 PRIOR APPLICATION NUMBER: 60/088876 PRIOR FILING DATE: 1998-06-11 PRIOR APPLICATION NUMBER: 60/0899105 PRIOR APPLICATION NUMBER: 60/089915 PRIOR APPLICATION NUMBER: 60/089440 PRIOR FILING DATE: 1998-06-16 PRIOR PRILING DATE: 1998-06-16 PRIOR APPLICATION NUMBER: 60/089512 PRIOR APPLICATION NUMBER: 60/089512 PRIOR APPLICATION NUMBER: 60/089512 PRIOR APPLICATION NUMBER: 60/089532 PRIOR FILING DATE: 1998-06-16 PRIOR APPLICATION NUMBER: 60/089538 PRIOR APPLICATION NUMBER: 60/089538 PRIOR APPLICATION NUMBER: 60/089538 PRIOR APPLICATION NUMBER: 60/089538 PRIOR APPLICATION NUMBER: 60/089539 PRIOR APPLICATION NUMBER: 60/089660 PRIOR PILING DATE: 1998-06-17 PRIOR APPLICATION NUMBER: 60/089699 PRIOR FILING DATE: 1998-06-17 PRIOR APPLICATION NUMBER: 60/089663 PRIOR APPLICATION NUMBER: 60/089669 PRIOR FILING DATE: 1998-06-18 PRIOR APPLICATION NUMBER: 60/089669 PRIOR FILING DATE: 1998-06-18 PRIOR APPLICATION NUMBER: 60/089663 PRIOR PILING DATE: 1998-06-18 PRIOR APPLICATION NUMBER: 60/089663 PRIOR APPLICATION NUMBER: 60/089663 PRIOR APPLICATION NUMBER: 60/089663 PRIOR PILING DATE: 1998-06-18 PRIOR APPLICATION NUMBER: 60/089663 PRIOR PILING DATE: 1998-06-18 PRIOR APPLICATION NUMBER: 60/089663 PRIOR PILING DATE: 1998-06-18 PRIOR APPLICATION NUMBER: 60/089663   | FILING DATE: 1998-06- APPLICATION NUMBER: 6 FILING DATE: 1998-06- |

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Gerber, Hanspeter
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Stewart,
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Eaton, Dan L.
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TITLE OF INVENTION: Secreted and Transmembra
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P23001C65
CURRENT APPLICATION NUMBER: US/09/989,727
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR PILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/065311
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PRIOR FILING DATE: 1998-10-2-25
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PRIOR APPLICATION NUMBER: 60/083600
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R FILING DATE: 1998-05-28

R FILING DATE: 1998-06-02

R APPLICATION NUMBER: 60/087609

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APPLICANT: Najari, red. 0.

APPLICANT: Najari, Ard. 0.

APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Roy, Margaret Ann
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.

APPLICANT: Stewart, Timothy A.

APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.

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PRIOR TILING DATE: 1998-07-07
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PRIOR FILING DATE: 1998-07-09
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APPLICANT: Baker,Kevin P.
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APPLICATION NUMBER: 60/090863
FILING DATE: 1998-06-26
APPLICATION NUMBER: 60/091360
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FILING DATE: 1998-06-18
APPLICATION NUMBER: 60/089907
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APPLICATION NUMBER: 60/091478
FILING DATE: 1998-07-02
APPLICATION NUMBER: 60/091544
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FILING DATE: 1998-06-25
APPLICATION NUMBER: 60/090695
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FILING DATE: 1998-06-23
APPLICATION NUMBER: 60/090429
FILING DATE: 1998-06-24
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APPLICATION NUMBER: 60/090349
FILING DATE: 1998-06-23
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APPLICATION NUMBER: 60/090252
FILING DATE: 1998-06-22
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FILING DATE: 1998-06-19
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APPLICATION NUMBER: 60/089908
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FILING DATE: 1998-06-25
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FILING DATE: 1998-06-24
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FILING DATE: 1998-06-24
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FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090472
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FILING DATE: 1998-06-19
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APPLICANT: Ashkenazi, Avi J.
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FILE REFERENCE: P2730P1C5/
CURRENT APPLICATION NUMBER: US/09/989,732
                                             APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C57
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OR FILING DATE: 1998-07-02
OR APPLICATION NUMBER: 60/091978
OR APPLICATION NUMBER: 60/091982
OR APPLICATION NUMBER: 60/091982
OR APPLICATION NUMBER: 60/092182
OR APPLICATION NUMBER: 60/092182
OR FILING DATE: 1998-07-09
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FILING DATE: 1998-07-02
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Grimaldi, J.Christopher
Gurney, Austin L.
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Stewart, Timothy A.
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Botstein, David
                                                                                                                                                                                                                                 Paoni, Nicholas F
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Pred. No. 0.092;
8; Mismatches 109;
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| 1998-<br>NUMBER | NUMBER | 1998-       | -RAGIT | NUMBER | 1998- | NUMBER | -BBBUN      | -RAGT | NUMBER | 1998- | NUMBER | 1998-           | NIMPER | 1998- | NIMBER | 1000 | NIMBER | NUMBER  | מממאוווו | -866 t | NIMBER | 1000- | NIMBER | NOMBER | TOCCT    | NOMBER | -8661 | NUMBER | 1998- | NUMBER | 1998-      | NUMBER       | - ROPL | 1998- | NUMBER | 1998- | NIMHER - | NUMBER | 1998- | NUMBER | 1998-      | -RAKT | NUMBER | 1998- | NUMBER                                  | NUMBER | 1998- | NUMBER      | 1998- | NUMBER | 1998- | NIMBER- | NUMBER | 1998- | NUMBER | -866T              | -866T            | TION NUMBER | DATE: 1998- | TITON NOMBER |
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DR APPLICATION NUMBER: 60/049787

R FILING DATE: 1997-06-16

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R APPLICATION NUMBER: 60/06226

R FILING DATE: 1997-11-13

R APPLICATION NUMBER: 60/066770

R FILING DATE: 1997-11-13

R APPLICATION NUMBER: 60/066770

R FILING DATE: 1997-11-24

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R APPLICATION NUMBER: 60/08322

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R APPLICATION NUMBER: 60/08760

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N NUMBER: 60/088826 E: 1998-06-10 N NUMBER: 60/088858 E: 1998-06-11 N NUMBER: 60/088861 E: 1998-06-11 N NUMBER: 60/08876 E: 1998-06-11 N NUMBER: 60/08976

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Patent No. US20020127576A1
GENERAL INFORMATION:
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R APPLICATION NUMBER: 60/091626
R FILING DATE: 1998-07-02
R APPLICATION NUMBER: 60/091633
R FILING DATE: 1998-07-02
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APPLICATION NUMBER: 60/091544
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APPLICATION NUMBER: 60/091519
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Baker, Kevin P.
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                                                                                Grimaldi, J.Christopher Gurney, Austin L. Kljavin, Ivar J.
                                                                                                                        Goddard, Audrey
Godowski, Paul
                                                                                                                                                  Gerber, Hanspeter
Gerritsen, Mary E.
                                                                                                                                                                                            Eaton, Dan L.
Ferrara, Napoleone
Tumas,
            Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy
                                                                                                                                                                                                                                 Botstein, David
                                                                                                                                                                               Fong, Sherman
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                                                        Pan,James
                                                                  Napier, Mary A.
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Pred. No. 0.092;
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PRIOR APPLICATION NUMBER: 60/049787
PRIOR APPLICATION NUMBER: 60/062250
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PRIOR APPLICATION NUMBER: 60/065186
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PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR PRIOR PRICING DATE: 1997-11-24
PRIOR PRIOR APPLICATION NUMBER: 60/075945
PRIOR PRIOR DATE: 1998-02-25
PRIOR PRIOR PRICING DATE: 1998-03-20
PRIOR PRIOR PRICING DATE: 1998-03-20
PRIOR PRICING DATE: 1998-03-20
PRIOR PRILING DATE: 1998-04-28
PRIOR PRILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/08706
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CURRENT FILING DATE: 2001-11-14
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Williams, P. Mickey
Wood, William I.
DATE:
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OR APPLICATION NUMBER: 60/091633

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OR APPLICATION NUMBER: 60/091978

OR FILING DATE: 1998-07-07

OR APPLICATION NUMBER: 60/091982

OR APPLICATION NUMBER: 60/092182

OR APPLICATION NUMBER: 60/092182

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OR APPLICATION NUMBER: 60/090695
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OR APPLICATION NUMBER: 60/090696
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APPLICATION NUMBER: 60/091519
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APPLICATION NUMBER: 60/091626
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FILING DATE: 1998-07-02
APPLICATION NUMBER: 60/091544
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                              Fong, Sherman
Gerber, Hanspeter
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Eaton, Dan L.
Ferrara, Napoleone
Gerritsen, Mary
Goddard, Audrey
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R FILING DATE: 1998-06-24

PR FPLICATION NUMBER: 60/990445

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PR APPLICATION NUMBER: 60/090472

PR APPLICATION NUMBER: 60/090535

PR FPLIC DATE: 1998-06-24

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APPLICATION NUMBER: 60/090435
FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090444

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60/090676

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APPLICATION NUMBER: 60/090540 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090542

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FILING DATE: 1998-06-22 APPLICATION NUMBER: 60/090254 FILING DATE: 1998-06-22 FILING DATE: 1998-06-22 APPLICATION NUMBER: 60/090252

DR APPLICATION NUMBER: 60/090349
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RR APPLICATION NUMBER: 60/089952

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PR FILING DATE: 1998-06-17

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PR APPLICATION NUMBER: 60/089653

PR FILING DATE: 1998-06-17

APPLICATION NUMBER: 60/089598 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089538 APPLICATION NUMBER: 60/089532

FILING DATE:

1998-06-17

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APPLICANT: Stewart,
APPLICANT: Tumas, Da
APPLICANT: Watanabe,
APPLICANT: Williams,
APPLICANT: Wood, Wil
APPLICANT: Zhang, Ze
TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REFERENCE: P2730
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CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
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Napier, Mary A.
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Sequence 517, Application US/09991163
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GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
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Pred. No. 0.092;
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and TITLE OF INVENTION: Acids Encoding the Same Fill REFERENCE: P2730PLC17

CURRENT PELLCATION NUMBER: US/09/991,163

CURRENT PILMG DATE: 1997-06-16

PRIOR PELLCATION NUMBER: 60/062250

PRIOR PELLCATION NUMBER: 60/062250

PRIOR PELLCATION NUMBER: 60/065311

PRIOR PELLCATION NUMBER: 60/075945

PRIOR PELLCATION NUMBER: 60/078910

PRIOR PELLCATION NUMBER: 60/08332

PRIOR PELLCATION NUMBER: 60/08332

PRIOR PELLCATION NUMBER: 60/08332

PRIOR PELLCATION NUMBER: 60/08760

PRIOR PELLCATION NUMBER: 60/088021

PRIOR PELLCATION NUMBER: 60/088025

PRIOR PELLCATION NUMBER: 60/088026

PRIOR PELLCA
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
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Godowski, Paul J.
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Gerritsen, Mary E
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Eaton, Dan L.
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FILING DATE: 1998-07-02
APPLICATION NUMBER: 60/091626
FILING DATE: 1998-07-02
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APPLICATION NUMBER: 60/090863
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APPLICATION NUMBER: 60/091360
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GSSRPPMQLDSTSAEDTSPALSSGSSKPRVSIPMVRILAPVLVLLSLLSAAGLIAFC
                           GSALPDPQ--TASALPDPPAASA-----
                                                      AQQTQPPGLTSPGLYPAATTAKQGKTGAEAPPLPGTSQYGHERTSQYTGTSPHPATSPPA
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FILING DATE: 1998-06-22
APPLICATION NUMBER: 60/090254
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NUMBER: 60/090429

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NUMBER: 60/089538 NUMBER: 60/089532 : 1998-06-17

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APPLICANT: William J. Mickey
APPLICANT: Wood, William I.
APPLICATION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PLC25
CURRENT APPLICATION NUMBER: US/09/93,604
CURRENT APPLICATION NUMBER: 60/049787
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/06216
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
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APPLICANT: Baker,Kevin P.
APPLICANT: Botstein,David
APPLICANT: Desnoyers,Luc
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APPLICATION NUMBER: 60/087609
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APPLICATION NUMBER: 60/066770
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APPLICATION NUMBER: 60/087607
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Williams, P. Mickey
Wood, William I.
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Gerritsen, Mary E.
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Ferrara, Napoleone
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APPLICATION NUMBER: 60/091626
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APPLICATION NUMBER: 60/091544
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RESULT 81
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PRIOR FILING DATE: 1997-11-12
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APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
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Gerritsen, Mary E
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Grimaldi, J. Christopher
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CURRENT APPLICATION NUMBER: US/09/989,721
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C55
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APPLICATION NUMBER: 60/088734
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CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C11
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Grimaldi, J. Christopher
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Botstein, David
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Kuo, Sophia S.
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ilarity 22.9%;
Conservative
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er, Hanspeter
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David L.
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Pred. No. 0.092;
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OR FILING DATE: 1997-11-13
OR APPLICATION NUMBER: 60/066364
OR FILING DATE: 1997-11-20
OR APPLICATION NUMBER: 60/077632
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OR APPLICATION NUMBER: 60/077641
OR APPLICATION NUMBER: 60/077640
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OR FILING DATE: 1998-03-31
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Best Local S
Matches 68
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C20
CURRENT APPLICATION NUMBER: US/09/992,598
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049/87
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58; Conservative
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Godowski, Paul J.
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Gerritsen, Mary E.
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Ferrara, Napoleone
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OR FILING DATE: 1998-06-10
OR APPLICATION NUMBER: 60/088742
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OR APPLICATION NUMBER: 60/088810
OR FILING DATE: 1998-06-10 DR FILING DATE: 1998-06-10

R APPLICATION NUMBER: 60/088858

DR FILING DATE: 1998-06-11

DR APPLICATION NUMBER: 60/088861

DR FILING DATE: 1998-06-11

DR APPLICATION NUMBER: 60/088876

DR APPLICATION NUMBER: 60/088876 FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088029
FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088030
FILING DATE: 1998-06-04 FILING DATE: 1998-06-02
APPLICATION UNMBER: 60/087609
FILING DATE: 1998-06-02
APPLICATION NUMBER: 60/087759
FILING DATE: 1998-06-02 FILING DATE: 1998-05-07
APPLICATION NUMBER: 60/0
FILING DATE: 1998-05-28
APPLICATION NUMBER: 60/0 FILING DATE: 1998-06-11 APPLICATION NUMBER: 60/ FILING DATE: 1998-06-12 APPLICATION NUMBER: 60/088824 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088826 FILING DATE: 1998-06-09
APPLICATION NUMBER: 60/088734
FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088738 FILING DATE: 1998-06-05 APPLICATION NUMBER: 60/0 FILING DATE: 1998-06-05 APPLICATION NUMBER: 60/0 APPLICATION NUMBER: 60/088033 FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/088326 APPLICATION NUMBER: 60/ FILING DATE: 1998-06-03 APPLICATION NUMBER: APPLICATION NUMBER: 60/075945 APPLICATION NUMBER: 60/066770 FILING DATE: 1997-11-24 FILING DATE: 1997-11-: APPLICATION NUMBER: 60 FILING DATE: 1997-10-17 APPLICATION NUMBER: 60/065186 APPLICATION NUMBER: 60/062250 FILING DATE: 1998-06-05 APPLICATION NUMBER: 60/088655 FILING DATE: 1998-06-05 APPLICATION NUMBER: 60/088202 APPLICATION NUMBER: FILING DATE: 1998-06-04 FILING DATE: 1998-00 APPLICATION NUMBER: APPLICATION NUMBER: 60/088026 FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/088025 APPLICATION NUMBER: APPLICATION NUMBER: 60/083322 APPLICATION NUMBER: FILING DATE: 1998-02-25 FILING DATE: 1997-11-DATE: 1998-06-04 DATE: 1998-04-28 DATE: 1998-03-20 NUMBER: 60/088217 1998-06-04 60/088212 60/088167 60/088028 60/088021 60/087827 60/087607 60/087106 60/084600 60/078910 60/065311

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58; Conservative
                                    Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
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                                                                                                                                                                                                                                                                                  Ashkenazi, Avi
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                                                                                                                                                                               Fong,
                                                                                                                         Gerritsen, Mary E. Goddard, Audrey
                                                                                                                                                    Gao, Wei-Qiang
Gerber, Hanspeter
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Botstein, David
                                                                                                                                                                                             Filvaroff, Ellen
Pan, James;
Paoni, Nich
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Eaton, Dan
                        Napier, Mary A.
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APPLICATION NUMBER: 60/090435 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090431

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FILING DATE: 1998-06-23
APPLICATION NUMBER: 60/090355
FILING DATE: 1998-06-23
APPLICATION NUMBER: 60/090429
FILING DATE: 1998-06-24

APPLICATION NUMBER: 60/090349 FILING DATE: 1998-06-23 APPLICATION NUMBER: 60/090254 FILING DATE: 1998-06-22

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DR APPLICATION NUMBER: 60/090472
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DR APPLICATION NUMBER: 60/090540

APPLICATION NUMBER: 60/090557 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090676

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APPLICATION NUMBER: 60/090542
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FILING DATE: 1998-06-25 APPLICATION NUMBER: 60/090678

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APPLICATION NUMBER: 60/089908 FILING DATE: 1998-06-18 APPLICATION NUMBER: 60/089947 FILING DATE: 1998-06-19 APPLICATION NUMBER: 60/089948

APPLICATION NUMBER: 60/090246
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APPLICATION NUMBER: 60/089952 FILING DATE: 1998-06-19

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APPLICATION NUMBER: 60/089801 FILING DATE: 1998-06-18 APPLICATION NUMBER: 60/089907 FILING DATE: 1998-06-18

APPLICATION NUMBER: 60/089653 FILING DATE: 1998-06-17

OR FILING DATE: 1998-06-17

OR APPLICATION NUMBER: 60/089598

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OR APPLICATION NUMBER: 60/089599

OR FILING DATE: 1998-06-17

OR APPLICATION NUMBER: 60/089600

OR FILING DATE: 1998-06-17

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APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Williams, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
ITILE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
ITILE OF INVENTION: Acids Encoding the Same
FILIE REFERENCE: P2630PLC27
CURRENT APPLICATION NUMBER: 09/09/978,697
CURRENT FILING DATE: 2001-07-10
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-31
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/065364
PRIOR APPLICATION NUMBER: 60/066364
PRIOR APPLICATION NUMBER: 60/077450
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
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DR APPLICATION NUMBER: 60/079920

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DR APPLICATION NUMBER: 60/078004
DR FILING DATE: 1998-03-13
DR APPLICATION NUMBER: 60/078886
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PR APPLICATION NUMBER: 60/080194

PR FILING DATE: 1998-03-31

PR APPLICATION NUMBER: 60/080327

PR FILING DATE: 1998-04-01

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FILING DATE: 1998-04-21 APPLICATION NUMBER: 60/082704 60/082569 60/082568 60/081838 60/081952

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APPLICATION NUMBER: 60/085323
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Baker, Kevin P.
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  Grimaldi
             Goddard, Audrey
Godowski, Paul
                                         Gerber, Hanspeter
Gerritsen, Mary E.
                                                                                  Eaton, Dan L.
Ferrara, Napoleone
                                                                                                             Desnoyers, Luc
                                                                     Fong, Sherman
                                                                                                                             Botstein, David
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WELLCANT: Zolia Control Tritle OF INVENTION: Scienced and Transmembrance Polypeptides and Nucleic Tritle OF INVENTION: Acids Encoding the Same

FILE REFERENCE: P27301666

CURRENT ELILAG DATE: 1997-06-16

FRIOR FILIAG DATE: 1997-06-16

FRIOR PELICATION NUMBER: 60/06220

FRIOR FILIAG DATE: 1997-10-17

FRIOR PELICATION NUMBER: 60/06220

FRIOR FILIAG DATE: 1997-10-17

FRIOR PELICATION NUMBER: 60/065311

FRIOR PELICATION NUMBER: 60/065311

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FRIOR PELICATION NUMBER: 60/065311

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FRIOR PELICATION NUMBER: 60/065311

FRIOR PELICATION NUMBER: 60/06530

FRIOR FRIING DATE: 1998-06-02

FRIOR PELICATION NUMBER: 60/06706

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Roy, Margaret Ann
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Kljavin, Ivar L
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DR APPLICATION NUMBER: 60/090676

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                                    GSALPDPO--TASALPDPPAASA----
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GSSRPPMQLDSTSAEDTSPALSSGSSKPRVSIPMVRILAPVLVLLSLLSAAGLIAFC
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Sequence 216, Application US/0, Patent No. US20020177553A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David RESULT 87 US-09-978-192A-216 US/09978192A

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FILE REFERENCE: ECURRENT APPLICATION OF PRIOR APPLICATION OF PRIOR APPLICATION OF THE PRIOR APPL
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OR FILING DATE: 1997-11-21
OR APPLICATION NUMBER: 60/077450
OR FILING DATE: 1998-03-10
OR APPLICATION NUMBER: 60/077632
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OR APPLICATION NUMBER: 09/918585
OR FILING DATE: 2001-07-30
OR APPLICATION NUMBER: 60/062250
OR FILING DATE: 1997-10-17
OR APPLICATION NUMBER: 60/064249
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OR FILING DATE: 1998-03-25
OR APPLICATION NUMBER: 60/079656
OR FILING DATE: 1998-03-26
OR APPLICATION NUMBER: 60/079664
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OR APPLICATION NUMBER: 60/079689
OR FILING DATE: 1998-03-27
OR APPLICATION NUMBER: 60/079663
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OR APPLICATION NUMBER: 60/079728
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R APPLICATION NUMBER: 60/078886

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DR APPLICATION NUMBER: 60/078936

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DR APPLICATION NUMBER: 60/078910

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Stewart,
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Gerritsen, Mary E.
Goddard, Audrey
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Williams, P. Mickey
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Hillan, Kenneth J
Kljavin, Ivar J.
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Grimaldi, J. Christopher
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ton, David L.
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f, Ellen
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                       GSALPDPQ--TASALPDPPAASA----
                                                                                                           LLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLE----
                                                                                                                                           SGTIYAEEEGQETMKGRVSIRDSRQEL----SLIVTLWNLTLQDAGEYWCGVEKRGPDES
                                                                                                                                                                 QGSFLT--KGPSKLNDRA---DSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQ
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GSSRPPMQLDSTSAEDTSPALSSGSSKPRVSIPMVRILAPVLVLLSLLSAAGLIAFC
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Pred. No. 0.092;
B; Mismatches 109;
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CURRENT APPLICATION NUMBER: 09/9199,832A
CURRENT FILING DATE: 09/916585
PRIOR APPLICATION NUMBER: 09/916585
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PRIOR APPLICATION NUMBER: 60/066364
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PRIOR PILING DATE: 1998-03-10
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PRIOR APPLICATION NUMBER: 60/078004
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TITLE OF INVENTION: Acids Encodi
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: Baker Kevin P.
: Botstein, David
: Desnoyers, Luc
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Goddard, Audrey
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Kuo, Sophia S.
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Grimaldi, J. Christopher
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SGTIYAEEEGQETMKGRVSIRDSRQEL----SLIVTLWNLTLQDAGEYWCGVEKRGPDES
                       LLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLE----
                                                                                                RLLVLLWGCLLLPGYEALEGPEEISGFEGDTVSLQCTYREELRDHRKYWCRKGGILFSRC
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APPLICATION NUMBER: 60/090431
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TITLE OF INVENTION: Secreted and Transmembra
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C19
CURRENT APPLICATION NUMBER: US/99/990,444
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/04987
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/06250
PRIOR APPLICATION NUMBER: 60/065186
PRIOR APPLICATION NUMBER: 60/06511
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
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Roy, Margaret Ann
Stewart, Timothy A
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Godowski, Paul J.
Grimaldi, J. Christopher
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Kljavin, Ivar J.
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Botstein, David
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N NUMBER: 60/087607 E: 1998-06-02 N NUMBER: 60/087609 E: 1998-06-02

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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C53
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Gerritsen, Mary E
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Ferrara, Napoleone
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FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089801

APPLICATION NUMBER: 60/089653

FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089600

APPLICATION NUMBER: 60 FILING DATE: 1998-06-1

60/089599 60/089598

APPLICATION NUMBER: 60/ FILING DATE: 1998-06-17

FILING DATE: 1998-06-18 APPLICATION NUMBER: 60/089947 FILING DATE: 1998-06-19

APPLICATION NUMBER: 60/090246

FILING DATE:

APPLICATION NUMBER: 60/089952 FILING DATE: 1998-06-19 APPLICATION NUMBER: 60/089948

1998-06-19

APPLICATION NUMBER: 60/090252 FILING DATE: 1998-06-22

1998-06-22

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RESULT 92
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APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembra
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C69
CURRENT APPLICATION NUMBER: US/09/989,730
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/04787
PRIOR FILING DATE: 1997-06-16
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OR FILING DATE: 1998-07-02
OR APPLICATION NUMBER: 60/091978
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l Similarity 22.9%;
68; Conservative 3
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: Baker, Kevin P.
: Botstein, David
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                                                                                                                   Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
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Gerber, Hanspeter
Gerritsen, Mary E.
                                                                                                                                                                  Tumas, Daniel
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Stewart, Timothy A.
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Kljavin, Ivar J.
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Grimaldi, J.Christopher
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b. US20020197674A1
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Pred. No. 0.092;
88; Mismatches 10
                                                                                         Transmembrane
                                                                            Same
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                                                                                             Nucleic
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PRIOR PRIOR

APPLICATION NUMBER: APPLICATION NUMBER: FILING DATE: 1998-0

60/090694

1998-06-25

60/090690

FILING DATE: 1998-06-24
APPLICATION UNMBER: 60/090676
FILING DATE: 1998-06-25
APPLICATION UNMBER: 60/090678
FILING DATE: 1998-06-25

R FILING DATE: 1998-06-25
R APPLICATION NUMBER: 60/99695
R FILING DATE: 1998-06-25
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R APPLICATION NUMBER: 60/090862
R FILING DATE: 1998-06-25
R APPLICATION NUMBER: 60/090862
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NUMBER: 60/091544 NUMBER: 60/091478

1998-07-02

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FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090542
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APPLICATION NUMBER: 60/090557

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APPLICATION NUMBER: 60/090535

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60/090472

APPLICATION NUMBER: 60/090435 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090444

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FILING DATE: 1998-06-23 APPLICATION NUMBER: 60/090429 FILING DATE: 1998-06-24 FILING DATE: 1998-06-23 APPLICATION NUMBER: 60/090355

APPLICATION NUMBER: 60/090431 FILING DATE: 1998-06-24

FILING DATE: 1998-0 APPLICATION NUMBER:

APPLICATION NUMBER: 60/090254

1998-06-22

60/090349

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NUMBER: 60:

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N NUMBER: 60/088029
TE: 1998-06-04
N NUMBER: 60/088030
FE: 1998-06-04
N NUMBER: 60/088033
N NUMBER: 60/088033
N NUMBER: 60/088326
N NUMBER: 60/088326

NUMBER: 60/088028: 1998-06-04

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60/088167

N NUMBER: 60/0 E: 1998-06-11 N NUMBER: 60/0 E: 1998-06-11 N NUMBER: 60/0 N NUMBER: 60/0

60/088861 60/088858

NUMBER: 60/0: 1998-06-10 NUMBER:

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NUMBER: 60/088738: 1998-06-10

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NUMBER: 60/088217 NUMBER: 60/ NUMBER: 60/088202

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60/088734 60/088655

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60/089105 60/088876 N NUMBER: 60/087759
TE: 1998-06-02
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NUMBER: 60/087609: 1998-06-02 NUMBER: 60/087607 : 1998-06-02

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60/088026 60/088025 N NUMBER: 60/075945
TE: 1998-02-25
N NUMBER: 60/078910
TE: 1998-03-20
TE: 1998-03-20
TE: 1998-04-28
TE: 1998-04-28
N NUMBER: 60/084600

NUMBER: 60/ : 1998-05-07

NUMBER: 60/ : 1998-05-28

60/087106

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; Sequence 517, Application US/(
publication No. US20020198148;
GENERAL INFORMATION:
APPLICANT: Ashkenazi,Avi J.
APPLICANT: Baker Kevin P.
APPLICANT: Botseain,David
APPLICANT: Desnoyers,Luc
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APPLICATION NUMBER: 60/091519
APPLICATION 1998-07-02
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FILING DATE: 1998-07-07
APPLICATION NUMBER: 60/092182
FILING DATE: 1998-07-09
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FILING DATE: 1998-06-26
APPLICATION NUMBER: 60/091360
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APPLICATION NUMBER: 60/091544
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65 QGSFLT--KGPSKLNDRA---DSRRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQ
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Roy, Margaret Ann
Stewart, Timothy F
Tumas, Daniel
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                                                                                                                  Godowski, Paul J.
Grimaldi, J.Christopher
Gurney, Austin L.
Kljavin, Ivar J.
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Gerber, Hanspeter
Gerritsen, Mary E.
                                                                                         Napier, Mary A.
Pan, James
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Ferrara, Napoleone
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Conservative 3
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art, Timothy A.
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Colin K.
P. Mickey
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38; Mismatches
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PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR PPLICATION NUMBER: 60/066770
PRIOR PPLICATION NUMBER: 60/066770
PRIOR APPLICATION NUMBER: 60/075945
PRIOR APPLICATION NUMBER: 60/079910
PRIOR PILING DATE: 1998-02-25
PRIOR PILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078910
PRIOR APPLICATION NUMBER: 60/083322
PRIOR APPLICATION NUMBER: 60/083322
PRIOR APPLICATION NUMBER: 60/084600
PRIOR APPLICATION NUMBER: 60/084600
PRIOR PILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR PILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-04-28
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C14
CURRENT APPLICATION NUMBER: US/09/990,436
CURRENT FILING DATE: 2001-11-14
                                         PRIOR

                                                                                                                                                                                                                                                                                                                                                                                                                              OR FILING DATE: 1998-06-05
OR APPLICATION NUMBER: 60/088202
OR FILING DATE: 1998-06-05
OR APPLICATION NUMBER: 60/088212
OR FILING DATE: 1998-06-05
OR APPLICATION NUMBER: 60/088217
OR APPLICATION NUMBER: 60/088217
OR APPLICATION NUMBER: 60/088655
OR APPLICATION NUMBER: 60/088655
OR FILING DATE: 1998-06-09
OR FILING DATE: 1998-06-09
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OR FILING DATE: 1998-05-28
OR APPLICATION NUMBER: 60/087607
OR FILING DATE: 1998-06-02
OR APPLICATION NUMBER: 60/087609
OR APPLICATION NUMBER: 60/087759
OR APPLICATION NUMBER: 60/087759
                                                                                                     DR FILING DATE: 1998-06-10

R APPLICATION NUMBER: 60/088742

DR FILING DATE: 1998-06-10

DR APPLICATION NUMBER: 60/088810

DR FILING DATE: 1998-06-10

DR APPLICATION NUMBER: 60/088824
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DR FILING DATE: 1998-06-04
DR APPLICATION NUMBER: 60/088028
OR FILING DATE: 1998-06-04
DR APPLICATION NUMBER: 60/088039
DR FILING DATE: 1998-06-04
DR FILING DATE: 1998-06-04
DR APPLICATION NUMBER: 60/088030
R FILING DATE: :
R APPLICATION NO
R FILING DATE: :
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APPLICATION NUMBER: 60/088021
FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088025
FILING DATE: 1998-06-04
                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/088734 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088738
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APPLICATION NUMBER: 60/088033
FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 1998-06 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088167
                                     NUMBER:
                                                                   1998-06-10
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Best Local S
Matches 68
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Publication No. US2002019814
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
                                                                                                                                                           APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                              APPLICANT:
APPLICANT:
APPLICANT:
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     APPLICANT:
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DR APPLICATION NUMBER: 60/090694

DR FILING DATE: 1998-06-25

DR APPLICATION NUMBER: 60/090695

DR FILING DATE: 1998-06-25

DR APPLICATION NUMBER: 60/090696
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APPLICATION NUMBER: 60/091633
FILING DATE: 1998-07-02
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APPLICATION NUMBER: 60/091519
FILING DATE: 1998-07-02
APPLICATION NUMBER: 60/091626
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FILING DATE: 1998-07-09
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FILING DATE: 1998-07-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/091978 FILING DATE: 1998-07-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QGSFLT--KGPSKLNDRA---DSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQ 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RLLVLLWGCLLLPGYEALEGPEEISGFEGDTVSLQCTYREELRDHRKYWCRKGGILFSRC
                                                                                                                                                                                                                                      Baker, Kevin P.
Botstein, David
Desnoyers, Luc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSALPDPQ--TASALPDPPAASA-----LPAALAVISFLLGLGVAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLE---- 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RHLLLVLQLALLPA--ATQGNKVVLGKKGDTVELTCTASQK-KSIQFHWKNSNQIKILGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AQQTQPPGLTSPGLYPAATTAKQGKTGAEAPPLPGTSQYGHERTSQYTGTSPHPATSPPA
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Goddard, Audrey
Godowski, Paul J.
Grimaldi, J.Christopher
Gurney, Austin L.
                                                                                                      Fong, Sherman
Gerber, Hanspeter
Gerritsen, Mary E.
                                                                                                                                                                                       Ferrara, Napoleone
                                                                                                                                                                                                                     Eaton, Dan L.
                                                                                                                                                                                                                                                                                                                                                                              Application US/09993687
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Pred. No. 0.092;
88; Mismatches 109;
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PRIOR PRIOR

APPLICATION NUMBER: 60/090472 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090535

APPLICATION NUMBER: 60/090445 FILING DATE: 1998-06-24

FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090435 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090444 FILING DATE: 1998-06-24

OR FILING DATE: 1998-06-24
OR APPLICATION NUMBER: 60/090540
OR FILING DATE: 1998-06-24
OR APPLICATION NUMBER: 60/90542
OR FILING DATE: 1998-06-24
OR APPLICATION NUMBER: 60/90557
OR APPLICATION NUMBER: 60/09057
OR APPLICATION NUMBER: 60/090676
OR APPLICATION NUMBER: 60/090676
OR APPLICATION NUMBER: 60/090678
OR FILING DATE: 1998-06-25
OR APPLICATION NUMBER: 60/090678
OR APPLICATION NUMBER: 60/090690
OR APPLICATION NUMBER: 60/090690

PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR

APPLICATION NUMBER: FILING DATE: 1998-00 APPLICATION NUMBER:

1998-06-23

60/090355 60/090349

APPLICATION NUMBER: 60/090252 FILING DATE: 1998-06-22 APPLICATION NUMBER: 60/090254 FILING DATE: 1998-06-22

FILING DATE: 1998-06-23
APPLICATION NUMBER: 60/090429
FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090431

PRIOR PRIOR PRIOR

OR APPLICATION NUMBER: 60/089908
OR FILING DATE: 1998-06-18
OR APPLICATION NUMBER: 60/089947
OR FILING DATE: 1998-06-19
OR APPLICATION NUMBER: 60/089948
OR FILING DATE: 1998-06-19
OR APPLICATION NUMBER: 60/089952
OR FILING DATE: 1998-06-19
OR APPLICATION NUMBER: 60/090246
OR FILING DATE: 1998-06-22

PRIOR PRIOR PRIOR PRIOR PRIOR

OR FILING DATE: 1998-06-17

R APPLICATION NUMBER: 60/089653

OR FILING DATE: 1998-06-17

OR APPLICATION NUMBER: 60/089801

OR FILING DATE: 1998-06-18

OR FILING DATE: 1998-06-18

OR FILING DATE: 1998-06-18

A APPLICATE: 1998-06-1,
DATE: 1998-06-1,
OR APPLICATION NUMBER: 60/089599
OR FILING DATE: 1998-06-17
IOR APPLICATION NUMBER: 60/089600
IOR APPLICATION NUMBER: 60/089653

.....BER: 60/089598 1998-06-17

1998-06-17

60/089538 60/089532

PRIOR PRIOR

NUMBER: 60/ : 1998-06-17 NUMBER:

APPLICATION N FILING DATE:

R FILING DATE:
R APPLICATION WIR FILING DATE:
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60/089514 60/089512 60/089440

1998-06-16

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FILING DATE:
APPLICATION N
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1998-06-1

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60/089105

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NUMBER: 60: 1998-06-1

1998-06-1

APPLICATION FILING DATE:

FILING DATE APPLICATION

1998-06-1

60/088876 60/088861 60/088858

CURRENT APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
TITLE OF IN
TITLE REFERE APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
APPLICANT: PRIOR
PRIOR OR APPLICATION NUMBER: 60/049787
OR FILING DATE: 1997-06-16
OR APPLICATION NUMBER: 60/062250
OR FILING DATE: 1997-10-17
OR APPLICATION NUMBER: 60/065186
OR FILING DATE: 1997-11-12 OR FILING DATE: 1997-11-24

OR APPLICATION NUMBER: 60/075945

OR FILING DATE: 1998-02-25

OR APPLICATION NUMBER: 60/078910

OR FILING DATE: 1998-03-20

OR APPLICATION NUMBER: 60/083322

OR APPLICATION NUMBER: 60/084600

OR APPLICATION NUMBER: 60/084600

OR APPLICATION NUMBER: 60/087106

OR APPLICATION NUMBER: 60/087106

OR APPLICATION NUMBER: 60/087106

OR FILING DATE: 1998-05-28

OR APPLICATION NUMBER: 60/087106

OR FILING DATE: 1998-05-28 DR FILING DATE: 1998-06-03

PR APPLICATION NUMBER: 60/088021

PR FILING DATE: 1998-06-04

PR APPLICATION NUMBER: 60/088025

PR FILING DATE: 1998-06-04

PR APPLICATION NUMBER: 60/088026

PR FILING DATE: 1998-06-04

PR APPLICATION NUMBER: 60/088028

PR APPLICATION NUMBER: 60/088029

PR FILING DATE: 1998-06-04

PR APPLICATION NUMBER: 60/088030

PR APPLICATION NUMBER: 60/088167

PR APPLICATION NUMBER: 60/0882020

PR APPLICATION NUMBER: 60/0882120

PR APPLICATION NUMBER: 60/08 E OF INVENTION: Secreted and Transmembrane Polypeptides and E OF INVENTION: Acids Encoding the Same REFERENCE: P2730P1C11 APPLICATION NUMBER: 60/065311 FILING DATE: 1997-11-13 APPLICATION NUMBER: 60/066770 PILING DATE: 1998-06-02
APPLICATION NUMBER: 60/087759
FILING DATE: 1998-06-02
APPLICATION NUMBER: 60/087827 APPLICATION NUMBER: 60/087607 FILING DATE: 1998-06-02 APPLICATION NUMBER: 60/087609 APPLICATION NUMBER: US/09/993,687 FILING DATE: 2002-11-14 Roy, Mar Stewart, Tumas, D Williams, P. Micl Wood, William I. Zhang, Watanabe, Paoni, Nicholas Kljavin, Ivar J. Napier, Mary A. Margaret Ann art, Timothy I Daniel Zemin Colin K. P. Mickey 70 A. Nucleic

PRIOR FILLING DATE: 1998-06-10
PRIOR PAPELICATION NUMBER: 60/088810
PRIOR FILLING DATE: 1998-06-10
PRIOR FILLING DATE: 1998-06-10
PRIOR PAPELICATION NUMBER: 60/088820
PRIOR PAPELICATION NUMBER: 60/088820
PRIOR APPLICATION NUMBER: 60/088861
PRIOR APPLICATION NUMBER: 60/088861
PRIOR APPLICATION NUMBER: 60/088861
PRIOR APPLICATION NUMBER: 60/089440
PRIOR APPLICATION NUMBER: 60/089512
PRIOR PILLING DATE: 1998-06-16
PRIOR PRILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089512
PRIOR PILLING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089539
PRIOR FILLING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089599
PRIOR FILLING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089599
PRIOR FILLING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089600
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PRIOR APPLICATION NUMBER: 60/089909
PRIOR APPLICATION NUMBER: 60/090246
PRIOR APPLICATION NUMBER: 60/090252
PRIOR APPLICATION NUMBER: 60/090439
PRIOR APPLICATION NUMBER: 60/090439

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RESULT 95
US-09-989-734-517
Sequence 517, Application US/(
Publication No. US20030003531.4
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David;
APPLICANT: Desnoyers, Luc
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R APPLICATION NUMBER: 60/990695

DR FILLING DATE: 1998-06-25

PR APPLICATION NUMBER: 60/090696

PR APPLICATION NUMBER: 60/090862

PR APPLICATION NUMBER: 60/090862

PR APPLICATION NUMBER: 60/090862

PR FILING DATE: 1998-06-26
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R APPLICATION NUMBER: 60/091519
R FILING DATE: 1998-07-02
R APPLICATION NUMBER: 60/091626
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R APPLICATION NUMBER: 60/091633
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APPLICATION NUMBER: 60/092182
FILING DATE: 1998-07-09
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APPLICATION NUMBER: 60/091982
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APPLICATION NUMBER: 60/090690
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APPLICATION NUMBER: 60/090678
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FILING DATE: 1998-06-24
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                                                                                                                                                                                                                                                       AQQTQPPGLTSPGLYPAATTAKQGKTGAEAPPLPGTSQYGHERTSQYTGTSPHPATSPPA
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Pred. No. 0.092;
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Pol
TITLE OF INVENTION: Secreted and Transmembrane Pol
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C64
CURRENT APPLICATION NUMBER: US/09/989,734
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR APPLICATION NUMBER: 60/06250
PRIOR FILING DATE: 1997-06-16
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APPLICATION NUMBER: 60/087759
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Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
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Stewart, Timothy
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OR FILING DATE: 1998-06-26
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OR APPLICATION NUMBER: 60/091360
OR FILING DATE: 1998-07-02
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OR APPLICATION NUMBER: 60/090445
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GSSRPPMQLDSTSAEDTSPALSSGSSKPRVSIPMVRILAPVLVLLSLLSAAGLIAFC 268
                                  GSALPDPQ--TASALPDPPAASA-----
                                                                         AQQTQPPGLTSPGLYPAATTAKQGKTGAEAPPLPGTSQYGHERTSQYTGTSPHPATSPPA
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Pred. No. 0.092;
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                                    -LPAALAVISFLLGLGLGVAC 252
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; Sequence 700, US20030004102A1
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CURRENT APPLICATION NUMBER: US/09/978,189
CURRENT APPLICATION NUMBER: 09/91858
PRIOR APPLICATION NUMBER: 09/91858
PRIOR FILING DATE: 2001-07-30
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/062250
PRIOR PILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/064249
PRIOR APPLICATION NUMBER: 60/06311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR APPLICATION NUMBER: 60/066364
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APPLICANT: Williams, P. Mickey
APPLICANT: William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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OR FILING DATE: 1998-03-20

R APPLICATION NUMBER: 60/079294

OR FILING DATE: 1998-03-25

OR FILING DATE: 1998-03-26

OR APPLICATION NUMBER: 60/079654

OR APPLICATION NUMBER: 60/079664

OR APPLICATION NUMBER: 60/079664

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R APPLICATION N
R FILING DATE:
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APPLICATION NUMBER: 60/077791
FILING DATE: 1998-03-12
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APPLICATION UNBER: 60/077450
FILING DATE: 1998-03-10
APPLICATION NUMBER: 60/077632
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APPLICATION NUMBER: 60/078936
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FILING DATE: 1998-03-13
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Shelton,
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Gerber, Hanspeter
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Hillan, Kenneth J
Kljavin, Ivar J.
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Grimaldi, J. Christopher
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                                                                                                                   NUMBER:
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PRIOR DA FILING DATE: 1998-04
NA APPLICATION NUMBER:
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OR FILING DATE: 1998-04-27

OR FILING DATE: 1998-04-27

OR APPLICATION NUMBER: 60/08

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OR APPLICATION NUMBER: 60/08

OR FILING DATE: 1998-04-29

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APPLICATION NUMBER: APPLICATION FILING DATE: 1998-03-31 APPLICATION NUMBER: 60/080194 FILING DATE: 1998-03-27 APPLICATION NUMBER: 60/079786 FILING DATE: 1998-04-22 APPLICATION NUMBER: 60/082796 FILING DATE: 1998-0 APPLICATION NUMBER: FILING DATE: 1998-04-FILING DATE: FILING FILING DATE: FILING DATE: FILING DATE: DATE: 1998-04-DATE: NUMBER: 60: 1998-04-0 NUMBER: NUMBER: NUMBER: NUMBER: NUMBER: NUMBER: 60/083495 NUMBER: 60/081955 NUMBER: 60/080334 1998-04-22 1998-04-15 1998-04-09 1998-04-09 1998-04-08 1998-04-01 1998-03-3 1998-03-30 1998-03-30 1998-03-27 1998-04-15 1998-04-15 1998-04-08 1998-04-08 1998-04-1998-04-01 1998-03-31 1998-04-22 1998-04-22 1998-04-08 1998-03-31 1998-04-2 60/081195 60/081071 60/080327 60/083392 60/083322 60/083336 60/082797 60/082700 60/082804 60/082704 60/082569 60/082568 60/081952 60/081819 60/081817 60/081229 60/081203 60/081049 60/081070 60/080333 60/080328 60/080165 60/080107 60/080105 60/079923 60/079920 60/079728 60/079663 60/079689

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FILING DATE: 1998-05-06
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APPLICATION NUMBER: 60/084366
FILING DATE: 1998-05-05
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APPLICATION I
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APPLICATION NUMBER: 60/084598
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                                                                                                                                             Score 125; DB
Pred. No. 0.092
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                 APPLICANT: ZHALEM
TITLE OF INVENTION: Secreted and Transmembra
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C38
CURRENT APPLICATION NUMBER: US/09/97,653
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR PELING DATE: 1997-10-17
PRIOR PELING DATE: 1997-11-12
PRIOR PELICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-12
PRIOR PELICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-12
PRIOR PELICATION NUMBER: 60/075945
PRIOR APPLICATION NUMBER: 60/075945
PRIOR APPLICATION NUMBER: 60/078910
PRIOR PILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/083322
PRIOR APPLICATION NUMBER: 60/083322
PRIOR APPLICATION NUMBER: 60/083322
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/087607
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APPLICANT: Ashkenaz
APPLICANT: Baker, K
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OR FILING DATE: 1998-05-07
OR APPLICATION NUMBER: 60/087106
OR FILING DATE: 1998-05-28
OR APPLICATION NUMBER: 60/087607
OR FILING DATE: 1998-06-02
OR APPLICATION NUMBER: 60/087609
OR FILING DATE: 1998-06-02
OR APPLICATION NUMBER: 60/087759
OR FILING DATE: 1998-06-02
OR APPLICATION NUMBER: 60/087827
OR APPLICATION NUMBER: 60/087827
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Goddard, Audrey
Goddowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
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Baker, Kevin P.
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Tumas, Daniel
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Williams, P. Mickey
Wood, William I.
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| HUBLICATION NO. US20030022187A1  GREARL INFORMATION: APPLICANT: Baker, Kevin P. APPLICANT: Baker, Kevin P. APPLICANT: Boctetin, David APPLICANT: Wolfies APPLICANTION WOMERS: WO/0993,667 APPLICANTION WOMERS: WO/0993,667 APPLICANTION WOMERS: WO/0993 APPLICANTION WOMERS: WO/ | 11 0006005  |
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
APPLICANT: Zhang, Zemin
ITILE OF INVENTION: Secreted and Transmembre
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C44
CURRENT APPLICATION NUMBER: US/09/97,428
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/049787
PRIOR APPLICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/062250
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Best Local S
Matches 68
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                                                            PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/0
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/0
PRIOR FILING DATE: 1997-11-13
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            OR APPLICATION NUMBER: 60/065186
OR FILING DATE: 1997-11-12
OR APPLICATION NUMBER: 60/065311
OR FILING DATE: 1997-11-13
OR APPLICATION NUMBER: 60/066770
OR APPLICATION NUMBER: 60/075945
OR APPLICATION NUMBER: 60/075945
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Roy, Margaret Ann
Stewart, Timothy A
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                                                                                                                                                                                                                                                                                                                                               Tumas,
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Grimaldi, J. Christopher
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Gerritsen, Mary E.
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DATE:
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b. US20030027162A1
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1998-02-25
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Pred. No. 0.092;
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| PRIOR APPLICATION PRIOR FILING DATE |
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| NUMBER: 60/09599 1998-06-17 NUMBER: 60/08960 1998-06-18 NUMBER: 60/089801 NUMBER: 60/089901 1998-06-18 NUMBER: 60/089908 1998-06-18 NUMBER: 60/089948 1998-06-19 NUMBER: 60/089948 1998-06-19 NUMBER: 60/090246 1998-06-29 NUMBER: 60/090252 1998-06-26 NUMBER: 60/090252 1998-06-26 NUMBER: 60/090429 NUMBER: 60/090429 NUMBER: 60/090429 NUMBER: 60/090429 NUMBER: 60/090429 NUMBER: 60/090431 1998-06-24 NUMBER: 60/090444 NUMBER: 60/090445 NUMBER: 60/090696   |

PRIOR

DR APPLICATION NUMBER: 60/078910
BR FILING DATE: 1998-03-20
BR FILING DATE: 1998-04-28
BR APPLICATION NUMBER: 60/08322
DR FILING DATE: 1998-05-07
DR APPLICATION NUMBER: 60/08760
DR FILING DATE: 1998-05-02
BR APPLICATION NUMBER: 60/08760
DR FILING DATE: 1998-06-02
DR APPLICATION NUMBER: 60/08760
DR FILING DATE: 1998-06-02
DR APPLICATION NUMBER: 60/08782
DR APPLICATION NUMBER: 60/08782
DR APPLICATION NUMBER: 60/08002
DR APPLICATION NUMBER: 60/08003
DR FILING DATE: 1998-06-04
DR APPLICATION NUMBER: 60/08020

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US-09-997-666-517
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P273091C42
CURRENT APPLICATION NUMBER: US/09/997,666
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/049787
PRIOR APPLICATION NUMBER: 60/062250
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OR FILING DATE: 1998-07-02
OR APPLICATION NUMBER: 60/091978
OR FILING DATE: 1998-07-07
OR APPLICATION NUMBER: 60/091982
OR FILING DATE: 1998-07-07
OR APPLICATION NUMBER: 60/092182
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Williams, P. Micke
Wood, William I.
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Tumas, Daniel
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Kljavin, Ivar J.
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Goddard, Audrey
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Botstein, David
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                                                                                                                                                                                                  Paoni, Nicholas F.
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o. US20030027163A1
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                                                                                                                                                                    Margaret Ann
art, Timothy A.
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                                                                                                                                 P. Mickey
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1998-06-19

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENT: PC-DOS/MS-DOS
SOFTWARE: PO-TUN-1995
LING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: US 07/927,931
PILING DATE: 07-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 41215-A-PC
TELECOMMUNICATION INFORMATION:
TELEPTAX: (212) 977-9809
TELEFAX: (212) 977-9809
TELEFAX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
PNOTED: ATO Amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6, Application US/08477460B Patent No. 6034223 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Progenice Pharmaceuticals, Inc.
TITLE OF INVENTION: NON-PEPTIDYL MOLETY-CONJUGATED
TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONJUGATES, AND USES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
               LENGTH: 310 amino
TYPE: amino acid
STRANDEDNESS: unkr
TOPOLOGY: unknown
                                                                310 amino acids
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US-09-770-014-94
US-09-100-409A-37
US-09-100-409A-35
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US-09-770-014-91
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Sequence 46, Appl
Sequence 2, Appli
Sequence 41, Appl
Sequence 60, Appli
Sequence 60, Appli
Sequence 8, Appli
Sequence 404, App
Patent No. 5171838
Sequence 47, Appl
Sequence 47, Appl
Sequence 47, Appl
Sequence 43, Appl
Sequence 43, Appl
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Sequence 93, Appl
Sequence 94, Appl
Sequence 96, Appl
Sequence 97, Appl
Sequence 97, Appl
Sequence 97, Appl
Sequence 97, Appl
Sequence 37, Appl
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Patent No. 6083478

GENERAL INFORMATION:
APPLICANT: Allaway, Graham P.
APPLICANT: Maddon, Paul J.
TITLE OF INVENTION: No. 6083478-Peptidyl Moiety-Conjugated CD4-Gamma2 and CD4-IgG2
TITLE OF INVENTION: No. 6083478-Peptidyl Moiety-Conjugated CD4-Gamma2 and CD4-IgG2
TITLE OF INVENTION: Immunoconjugates and Uses Thereof

FILE REFERENCE: 41215-A-PCT-US
CURRENT APPLICATION NUMBER: US/08/379,516

CURRENT APPLICATION NUMBER: PCT/US93/07422

EARLIER APPLICATION NUMBER: PCT/US93/07422

EARLIER APPLICATION NUMBER: PCT/US93/07422

EARLIER APPLICATION NUMBER: 07/927,931

EARLIER APPLICATION SUMBER: 07/927,931

EARLIER FILING DATE: 1992-08-07

NUMBER OF SEQ ID NOS: 9

SOFTWARE: PatentIn Ver. 2.1

FEG ID NO 6
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; ORGANISM: home
; CELL TYPE: lyn
US-08-477-460B-6
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Best Local Similarity 85.,
209; Conservative
                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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                   TWTCTVLQNQKKVEFKIDIVPRASALPAPPTGSALPDPQTASALPDPPAASALPAALAVI
                                                                LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
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TWTCTVLQNQKKVEFKIDIVVLAFTVAAP-
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85.7%;
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Pred. No. 3.5e-80;
4; Mismatches 19
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Pred. No. 3.5e-80;
4; Mismatches 19
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REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 4121
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEPAX: (212) 977-9809
TELEFAX: (212) 977-9809
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: 08/477
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 07/
FILING DATE: 07-AUG-1992
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPUTER: COMPUTER: PM PC COMPUTER: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
ORIGINAL SOURCE:
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TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED
TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONJUGATES, AND USES THEREOF
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                                                                                                                                                                                                                                                                          Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                 CELL TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: unknown
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                                                                                                                                                                                                                                                                                                                                                                    ORGANISM:
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                                                           LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180
                                                                                                                                 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
                                                                                                                                                                                   MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
                                    LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180
                                                                                                          ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
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30 Rockefeller Plaza
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85.7%;
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Pred. No. 3.5e-80;
4; Mismatches 19;
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                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/476,227
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REGISTRATION NUMBER: 37690-I
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Beaudry, (
APPLICANT: Maddon, Partitle OF INVENTION: (
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.24 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                        Match 78.8%;
Local Similarity 85.7%;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 310 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
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ZIP: 10036
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                                                                                                                                                                                                                                                                                                                                                  ORGANISM:
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181 TWTCTVLQNQKKVEFKIDIVPRASALPAPPTGSALPDPQTASALPDPPAASALPAALAVI 240
                                  121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
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Pred. No. 3.5e-80;
4; Mismatches 19
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                                                                                                                                                                                                                                                                               DB 3;
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                                                                                                                                                                                                                                                                            Length 310;
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US-09-409-006A-6
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TELEPHONE: (212) 977-9550
TELEFAX: (212) 977-9809
TELEFAX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
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Patent No. 6342586
                                                                                                                                                                                                                         Matches 209;
                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/927,931
FILING DATE: 07-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41215-A-PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
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TITLE OF INVENTION: N
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CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                      ORGANISM:
CELL TYPE:
                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: unl
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                                                        LVFGLTANSDTHLLQGQSLTLTLESSPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180
                                                                                                               ILGNQGSFLTKGPSKLNDRADSRRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
TWTCTVLQNQKKVEFKIDIVPRASALPAPPTGSALPDPQTASALPDPPAASALPAALAVI 240
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NON-PEPTITYL MOIETY-CONJUGATED
CD4-GAMMA2 AND CD4-IGG2 IMMUNOCONJUGATES, AND USES THEREOF
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85.7%;
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Pred. No. 3.5e-80;
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RESULT 6
US-08-484-681-6
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Best Local Similarity 85.7%;
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SEQUENCE CHARACTERISTICS:
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NAME: White, John P.
REGISTRATION NUMBER: 28,678
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
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ORIGINAL SOURCE:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
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MEDIUM TYPE: Floppy
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper &
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                   TWTCTVLQNQKKVEFKIDIVPRASALPAPPTGSALPDPQTASALPDPPAASALPVI
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1185 Avenue of the Americas
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                        Score 1038; DB 4;
Pred. No. 3.5e-80;
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                                                                                                                                                                                                                                                                                                            DB 4;
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PCT-US93-07422-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 4121
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9850
TELEFAK: (212) 977-9809
TELEFAK: 42552 COOP UI
INFORMATION FOR SEQ ID NO: 6:
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GENERAL INFORMATION:
APPLICANT: Proger
                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                           Matches 209;
                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: homo sapier
CELL TYPE: lymphocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 310 amino acid
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PRIOR APPLICATION NUMBER: US 07/927,931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 0 FILING DATE: 07-AUG-1992 ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
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                              TWTCTVLQNQKKVEFKIDIVVLAFTVAAP--
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85.7%;
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Pred. No. 3.5e-80;
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                              SVFIFPPSDEQLKSGTASV 228
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US-08-477-460B-2
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Patent No. 6034223
GENERAL INFORMATION:
APPLICANT: Progenics Pharmaceuti
                                                                                                                                                                                                                                                                                                Matches 206;
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                                                                                                                                                                                                                                                                                                                  Best Local Similarity
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TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/477,460B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/927,931
APPLICATION OF AUG-1992
ATTORNEY/ACENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
ORIGINAL SOURCE:
ORGANISM: hom
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TELECOMMUNICATION INFORMATION:
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: White, John P. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                           CELL TYPE:
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                           TWTCTVLQNQKKVEFKIDIV----PRASALPAPPTGSALPDPQTASALPDPPAA 230
                                                                       LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
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30 Rockefeller Plaza
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VENTION: NON-PEPTIDYL MOIETY-CONJUGATED
VENTION: CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONJUGATES,
                                                                                                                                                                                                                                                                                              Conservative
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88.0%;
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Pred. No. 1.6e-79;
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-CPAPPVA 221
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US-09-329-916-2
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CURRENT FILING DATE: 1996-06-10
EARLIER APPLICATION NUMBER: PCT/US93/07422
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EARLIER APPLICATION NUMBER: 07/927,931
EARLIER FILING DATE: 1992-08-07
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.1
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ORGANISM: Homo sapiens
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                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/4
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                         MEDIUM TYPE: Floppy
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TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED
TITLE OF INVENTION: CD4-GAMMAZ AND CD4-IGG2 IMMUNOCONJUGATES, AND USES THEREOF
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                         STREET: 30 Rocke
CITY: New York
STATE: New York
                                                            CLASSIFICATION:
                                                                                    FILING DATE:
                                                                                                       APPLICATION NUMBER: US/09/329,916
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RESULT 11
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US-09-329-916-2
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APPLICANT: Beaudry,
APPLICANT: Maddon,
TITLE OF INVENTION:
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TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.24 CURRENT APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/4
FILING DATE: 07-JUN-1995
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ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                           STREET: Lit.
STREET: New York
STRY: New York
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CORRESPONDENCE ADDRESS:
ATTORNEY/AGENT INFORMATION:
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                                                                                                     APPLICATION NUMBER:
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STRANDEDNESS: un
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88.0%;
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                                  08/476,227
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                                                                                                   US/08/485,372A
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Pred. No. 1.6e-79;
1; Mismatches 10
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US-09-409-006A-2
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Best Local Sim
Matches 206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/09409006A Patent No. 6342586
                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/409,006A
FILING DATE: 29-SEP-1999
CLASSIFICATION: 424
                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/927,931
FILING DATE: 07-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41215-A-PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Progenics
TITLE OF INVENTION: N
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                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
 TELECOMMUNICATION INFORMATION:
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CELL TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (212) 391-0525
TELEX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                  CITY: New York
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                                                                                                                                                                                                                                                                                                                              COUNTRY:
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                                                                                                                                                                                                                                                                                                                              USA
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: lymphocyte
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88.0%;
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NON-PEPTIDYL MOIETY-CONJUGATED
CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONJUGATES, AND USES THEREOF
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                  41215-A-PCT/JPW/AJM
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Pred. No. 1.6e
1; Mismatches
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US-08-484-681-2
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GENERAL INFORMATION:
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                                   INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 37/
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                             SOFTWARE: PATENTIN Release #1.24
CURRENT APPLICATION INSTR:
APPLICATION NUMBER: US/08/484,681
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: (CORRESPONDENCE ADDRESS: Cooper &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Beaudry, Gar
APPLICANT: Maddon, Paul
TITLE OF INVENTION: CD4
                                                                                      TELEFAX:
                                                                                                           TELEPHONE:
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amino acid
                432 amino acids
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                                                                                        (212)
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Gary A. Paul J.

CD4-GAMMA2 CD4-IgG2 CHIMERAS

unknown

391-0525 278-0400

37690-II-B

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TELEFAX: (212) 977-9809
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 432 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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                      181 TWTCTVLQNQKKVEFKIDIV----PRASALPAPPTGSALPDPQTASALPDPPAA 230
                                                                                  121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180
                                                                                                                121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
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                                                                                                                                                                                                                                                                                                   1 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
TWTCTVLQNQKKVEFKIDIVVLAFERKCCVECPP------CPAPPVA 221
                                                                                                                                                                                                     ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
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88.0%;
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Pred. No. 1.6e-
1; Mismatches
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PCT-US93-07422-2
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION UNMBER: PCT/US93/07422
FILING DATE: 19930806
                                                                                                                                           REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEPAX: (212) 977-9809
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                  MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 07-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Progenics Pharmaceuticals, Inc.
TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED
TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IGG2 IMMUNOCONJUGATES, AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ORGANISM: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: New York
STATE: New York
                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                            TOPOLOGY:
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30 Rockefeller Plaza
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                   homo sapien
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88.0%;
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Pred. No. 1.6e
1; Mismatches
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                                                         US-08-477-460B-4
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 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/477,460B
FILING DATE: 07-UN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/927,931
FILING DATE: 07-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41115-A-PCT,
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Progenics Pharmaceuticals, Inc.
TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED
TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IGG2 IMMUNOCONJUGATES, AND USES THEREOF
                                                                                                                                                                                                                                        TELEX: 422523 COOP UI
                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 530 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
                                                                                                            MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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ADDRESSEE: Cooper &
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                                                                        ORGANISM:
CELL TYPE:
                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                      TYPE:
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212) 977-9809
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Pred. No. 1.6e-79;
Score 1030.5; DB 3; Pred. No. 3.1e-79;
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US-08-379-516-4
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RESULT 17
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Best Local Simi
Matches 207;
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APPLICANT: Maddon, Paul J.

TITLE OF INVENTION: No. 6083478-Peptidyl Moiety-Conjugated CD4-Gamma2 and CD4-IgG2
TITLE OF INVENTION: Immunoconjugates and Uses Thereof
FILE REFERENCE: 41215-A-PCT-US
CURRENT TAPPLICATION NUMBER: US/08/379,516
CURRENT TILING DATE: 1996-06-10
EARLIER APPLICATION NUMBER: PCT/US93/07422
EARLIER APPLICATION NUMBER: 07/927,931
EARLIER FILING DATE: 1992-08-07
EARLIER FILING DATE: 1992-08-07
NUMBER: OF SEQ ID NOS: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 4
LENGTH: 530
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Patent No. 6083478
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Local Similarity 84.8%;
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Pred. No. 3.1e.
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CELL TYPE:
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Sequence 4, Application US/09329916 Patent No. 6177549
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APPLICATION NUMBER: 08/477,460

FILING DATE: 07-JUN-1995

APPLICATION NUMBER: US 07/927,931

FILING DATE: 07-AUG-1992

ATTORNSY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 41215-A-PC

TELEPHONE: (212) 977-9550

TELEPAX: (212) 977-959
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Progenics Pharmaceuticals, Inc.
TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED
TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONJUGATES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 9
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: unl
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241 SFLL 244
                                                                                                                              121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
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Similarity 84.8%;
                                                                  TWTCTVLQNQKKVEFKIDIVPRASALPAPPTGSALPDPQTASALPDPPAASALPAALAVI
                                                                                                                                                     LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180
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                                         TWTCTVLQNQKKVEFKIDIVVLAFASTKGP--
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lymphocyte
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                                           SVFPLAPCSRSTSESTAAL
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US-08-485-372A-4
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Patent No. 6187748
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Best Local Similarity
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 37
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/476,227
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.24 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/485,37
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APPLICANT: Maddon, Paul J.
TITLE OF INVENTION: CD4-GAMMA2 CD4-IgG2 CHIMERAS
NUMBER OF SEQUENCES: 9
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STRANDEDNESS: unl
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                               241 SFLL 244
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GCLV 233
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84.8%;
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Pred. No. 3.1e-79;
5; Mismatches 21;
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                                                                   SVFPLAPCSRSTSESTAAL
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US-09-409-006A-4
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US-09-409-006A-4
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GENERAL INFORMATION:
APPLICANT: Progenics Pharmaceuti
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Best Local Similarity
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/927,931
FILING DATE: 07-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41215-A-PC
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (212) 977-9550
TELEFAX: (212) 977-9809
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Progenics Pharmaceuticals, Inc.
TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED
TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONJUGATES,
                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.24
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                               241 SFLL 244
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230 GCLV 233
                                                                                            181 TWTCTVLQNQKKVEFKIDIVPRASALPAPPTGSALPDPQTASALPDPPAASALPAALAVI
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Pred. No. 3.1e.
5; Mismatches
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                                                               -SVFPLAPCSRSTSESTAAL
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US-08-484-681-4
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Best Local Similarity
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,681
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 37690-II-B
TELEPHONE: (212) 278-0400
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APPLICANT: Maddon, Paul J.
TITLE OF INVENTION: CD4-GAMMA2 CD4-IgG2 CHIMERAS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: homo sapien
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: unl
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230 GCLV 233
                                   241 SFLL 244
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                                                                                                                                                                                                                                                                                                              MNRGVPFRHILLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKS1QFHWKNSNQIK 60
                                                                                                                                          LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180
                                                                                                                                                                                                                ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
                                                                                                      TWTCTVLQNQKKVEFKIDIVPRASALPAPPTGSALPDPQTASALPDPPAASALPAALAVI 240
                                                                       TWTCTVLQNQKKVEFKIDIVVLAFASTKGP--
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1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                       lymphocyte
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84.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                  DB 4; Length 530;
                                                                                                                                                                                                                                                                                                                                                                21;
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                                                                      SVFPLAPCSRSTSESTAAL 229
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RESULT 21 PCT-US93-07422-4

RESULT 22 US-08-284-391B-31 ; Sequence 31, App

Application US/08284391B

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GENERAL INFORMATION:
APPLICANT: Progenics Pharmaceuticals, Inc.
TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED
TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IgG2 IMMUNOC
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity Matches 207; Conserva
                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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TELEX: 422523 COOD UI
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/927,931

FILING DATE: 07-AUG-1992

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 41215-A-PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (212) 977-9550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 19930 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM:
CELL TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 530 amino acids
                                 241 SFLL 244
                                                                     181 TWTCTVLQNQKKVEFKIDIVVLAFASTKGP
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                                                                                                                                          121
                                                                                                                                                              121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180
230 GCLV 233
                                                                                                                                                                                                             61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
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lymphocyte
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84.8%;
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Pred. No. 3.1e-79;
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                                                                       -SVFPLAPCSRSTSESTAAL
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RESULT 23
US-09-218-950-31
; Sequence 31, Application US/09218950
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Best Local Similarity
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APPLICANT: Banapour, Babak
APPLICANT: Romeo, Charles
APPLICANT: Kolanus, Waldemar
TITLE OF INVENTION: TARGETED C
TITLE OF INVENTION: CELLS BY C
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/284,391B
FILING DATE: 02-AUG-1994
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Elbing, Karen L
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 07/847,566
FILING DATE: 06-MAR-1992
APPLICATION NUMBER: 07/665,961
FILING DATE: 07-MAR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/1
FILING DATE: 14-FEB-1994
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TELEFAX: 617-428-7045
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENGTH: 203 amino acids
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                                                                                                                                                                                                        121 LVFGLTANSDTHLLQGQSLTLTLESSPGSSSPSVQCRSSPRGKNIQGGKTLSVSQLELQDSG 180
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                                                                                                                                       TWTCTVLQNQKKVEFKIDIV 200
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                                                                                                                                                                             LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180
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                                                                                                  TWICTVLQNQKKVEFKIDIV 200
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176 Federal Street
                                                                                                                                                                                                                                                                                                                                                                                                                   78.1%; Score 1029; DB 2; ilarity 100.0%; Pred. No. 1.1e-79; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IBM Compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08/195,395
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GENERAL INFORMATION:
APPLICANT: Seed,
APPLICANT: Banapo
                                                                                                                                                                                                                                                                                                 Matches 200;
                                                                                                                                                                                                                                                                                                                    Best Local
                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY JAGENT INFORMATION:
NAME: Elbing, Karen L
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 0078
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Banapour, Babak
APPLICANT: Romeo, Charles
APPLICANT: Kolanus, Waldemar
TITLE OF INVENTION: TARGETED CYTOLYSIS OF HIV-INFECTED
TITLE OF INVENTION: CELLS BY CHIMERIC CD4 RECEPTOR- BEARING CELLS
NUMBER OF SEQUENCES: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 02-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FBStCSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: 1i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS LENGTH: 203 amino aci
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FILING DATE: 14-FEB-1994
APPLICATION NUMBER: 07/847,566
FILING DATE: 06-MAR-1992
APPLICATION NUMBER: 07/665,961
FILING DATE: 07-MAR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 203 amino acids
TYPE: amino acid
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181
                                                                         121
                                                                                                          121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                 61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
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TWTCTVLQNQKKVEFKIDIV 200
                           TWTCTVLQNQKKVEFKIDIV 200
                                                                       LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
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                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: DOS
SOFTWARE: FASESEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/284,391B
FILING DATE: 02-AUG-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 08/195,395
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: 07/847,566
FILING DATE: 06-MAR-1992
APPLICATION NUMBER: 07/665,961
FILING DATE: 07-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: R1bing. Karen L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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TOPOLOGY: lin
MOLECULE TYPE:
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APPLICANT: Banapour, Babak
APPLICANT: Romeo, Charles
APPLICANT: Kolanus, Waldemar
TITLE OF INVENTION: TARGETED CYTOLYSIS OF HIV-INFECTED
TITLE OF INVENTION: CELLS BY CHIMERIC CD4 RECEPTOR- BEARING CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Elbing, Karen L
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM CON
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 617-428-7045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
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                                                                                                           LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
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                           TWTCTVLQNQKKVEFKIDIV 200
                                                                        LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
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TWTCTVLQNQKKVEFKIDIV 200
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                                                                                                                                                                                                                                                                                                78.1%; Score 1029; DB 2; ilarity 100.0%; Pred. No. 2.8e-79; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                             linear
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RESULT 25

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Patent No. 63
                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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FILLING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US/08/284,391
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SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Elbing, Karen L
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617.428-0200
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APPLICANT: Romeo, Charles
APPLICANT: Kolanus, Waldemar
TITLE OF INVENTION: TARGETED CYTOLYSIS OF HIV-INFECTED
TITLE OF INVENTION: CELLS BY CHIMERIC CD4 RECEPTOR- BEARING CELLS
NUMBER OF SEQUENCES: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 07/6
FILING DATE: 07-MAR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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FILING DATE: 02-AUG-1994
APPLICATION NUMBER: 08/195
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: 07/847
FILING DATE: 06-MAR-1992
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                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
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 181 TWTCTVLQNQKKVEFKIDIV 200
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                                                                      121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180
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US-08-236-311-1
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                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 07/104329
FILING DATE: 02-OCT-1987
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 07/250785
FILING DATE: 28-SEP-1988
PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
FILING DATE: 26-AUG-
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PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US
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APPLICANT: Gregory, Timothy J.
TITLE OF INVENTION: Adheson Variants
NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: 07/842777
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                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 44
                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 402 amino TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 02-MAY-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                             121 LVFGLTANSDTHLLQGQSLTLITLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180
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                   TWTCTVLQNQKKVEFKIDIV 200
                                                                                                                                             ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
                                                                                                                                                                  ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
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                                                                      LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
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415/952-9881
                                                                                                                                                                                                                                                                                     78.1%; Score 1029; DB 1; ilarity 100.0%; Pred. No. 2.8e-79; Conservative 0; Mismatches
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US-08-457-918-1
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                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Capon, Daniel J.
APPLICANT: Gregory, Timothy J.
TITLE OF INVENTION: Adheson Variants
NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 402 amino acids
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PRIOR APPLICATION DATA:
08/236311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Kubinec, Jeffrey S:
REGISTRATION NUMBER: 36,5
REFERENCE/DOCKET NUMBER:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 18-FEB-
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 28-SEP-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
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TELEFAX: 910/371-7168
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 07/104329 FILING DATE: 02-OCT-1987
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                                                       121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
181 TWTCTVLQNQKKVEFKIDIV 200
                               121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
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